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Copyright (c) 1993 - 2004 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

REFER	KEYWORDS SOURCE ORGANI	LOCUS DEFINITION ACCESSION VERSION	RESUL		O 14 - 44	4.4	0 0 4 4	4.	ຸມພ	ი ი ა ა	, w	w w	α ω ι	(	0	, N	NN	s Ks	00	a N	10			, r	<b>-</b>	. ب	, o c							Result
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CUS FINITION CESSION RSION YWORDS URCE	AX671525 Sequence 4 from Patent WO03004652.  AX671525 AX671525.1 GI:29329875 Bacillus thuringiensis
RSION YWORDS	AX671525.1 GI:29329875
ÜRCE	Bacillus thuringiensis
ORGANISM	Bacillus thuringiensis Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
	cereus group.
AUTHORS	Stewart, F.A., Zhang, Y. and Hallet, B.
JOURNAL	Patent: WO 03004652-A 4 16-JAN-2003;

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The European Molecular Biology Laboratory (DE) ; L'Universite
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Mahillon, J. and Lereclus, D.
Structural and functional analysis of Th4430: identification of an integrase-like protein involved in the co-integrate-resolution
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transposon; unidentified r
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Baci
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                                     Submitted (24-MAR-1998) Hoflack L., Plant Gene Plateaustraat 22, B-9000 Gent, Belgium On Jun 2, 1998 this sequence version replaced
                                                                                                                                     Submitted (04-NOV-1988) Mahillon J., Plant Genetics Systems, Plateaustraat 22, B-9000 Gent, Belgium revised by [3]
3. (bases 1 to 9672)
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Mahillon, J. and Seurinck, J.
Mahillon, J. and Seurinck, J.
Complete nucleotide sequence of pGI2, a Bacillus thuringiensis
plasmid containing Tn4430
Nucleic Acids Res. 16 (24), 11827-11828 (1988)
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Bacillus thuringiensis plasmid i
X13481 GI:3171732
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                                                                                                                        Hoflack,
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Location/Qualifiers
1. .9672
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Pred. No. 1.4e-31;
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TGECI I RSGKGGKQR I VLLNSKVLSA I KDYLI DRKTYSTAHESPYLF I SKKREKLDR I
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|93. .497
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                                         Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales;
                                                                                                          Sequence 2 from Patent W003004652
AX671523
AX671523.1 GI:29329873
Stewart, F.A.,
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TKTEVTTKLFGKPEITEKKTGNIVVTBAQWRDMTEKVNAAVIVKDYERLQKTDLVKE
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VLYQQTKKVFKEQFKAFRGLIKNELDMKGVDNQFEREHTREIRSRQKGYDMER"
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KNPTYCSKLVFQALYFGSGSRNVMQAVSGIVTPYGLIDTFTSAYRPSLVKTY"
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/protein_id="CAA31835.1"
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/db_xref="GI:40321"
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Zhang, Y. and
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                                                                                               Sequence 8 from AX671529
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Use of a tyrosine recombinase for genetic engineering
Patent: WO 03004652-A 7 16-JAN-2003;
The European Molecular Biology Laboratory (DE); L'Un:
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Sequence 7 from Patent WO03004652
AX671528 GI:29329878
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Bacillus thuringiensis
Bacteria; Firmicutes;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bacillus thuringiensis"
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/db_xref="taxon:1428"
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/db_xref="taxon:1428"
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Pred. No. 5.8e-10;
                  Bacillales;
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The European Molecular Biology Laboratory Catholique De louvain (BE)
Location/Qualifiers
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Location/Qualifiers
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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from Patent WO03004652.
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falciparum 3D7
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Submitted (25-UNN-2001) Junichi Watanabe, Institute of Medical Science, The University of Tokyo, Department of Parasitology; Shirokanedal, Minatoku, Tokyo 108-8639, Japan (E-mail:jwatanab@manage.ims.u-tokyo.ac.jp, URL:http://fullmal.ims.u-tokyo.ac.jp, Tel:81-3-5449-5291,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe,J., Sasaki,M., Suzuki,Y. and Sugano,S. FULL-malaria: a database for a full-length enriched from human malaria parasite, Plasmodium falciparum Nucleic Acids Res. 29 (1), 70-71 (2001)
Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Api
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/protein_id="BAB79691.1"
/db_xref="GI:18143613"
/translation="MAGTSEAVKKWVNKIIEENIIAVFAKTECPYCIKAISILKGYNL
NSHMHYENIEKNPDMANIQAYLKELIGKSSVFRIFINKDVVGGCDDLVKENDEGKLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On or before Aug 30, 2001 this sequence version replaced gi:2982545, gi:2982549, gi:2982546, gi:2982548, gi:2982548, gi:2982548, gi:2982519, gi:2982580, gi:298487, gi:265315, gi:2982565, gi:2982578, gi:2982517, gi:2982518, gi:2982519, gi:4993878.
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Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
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Nature 419 (6906), 527-531 (2002)
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Location/Qualifiers
score 66.70, E-value 4.8e-16
Similiar to Plasmodium vivax pvlh14090, p pvlh14090W
SWALL:AAF99464 (EMBL:AY003872) (611 aa) fasta score
5.6e-172, 71.94% id in 613 aa, and to Mus musculus
5033406114rik protein 5033406114rik SWALL:Q993Q8
(EMBL:AK017158) (368 aa) fasta scores: E(): 1.7e-08
                                                                                                                                                                                                                  4 weak Pfam matches to entry PF00023 ank, match to entry PF01529 zf-DHHC, DHHC zinc score 66.70, E-value 4.8e-16
                                                                                                                                                                                                                                                                                                                                                                                        join(1030..2337,2429..2502,2645..2685,28265..2941,
3046..3173,3308..3388,3508..3571,3699...3737)
/genne="MALJ3P2.1"
/note="Revised: revised to 8 exon structure, revised:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(1030. .2337,2429. .2502,2645. .2685,2826. .2941,
3046. .3173,3308. .3388,3508. .3571,3699. .3737)
/gene="MAL3P2.1"
                                                                                                                                                                                                                                                                                                                                                   donor for exon 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:36329"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="synonym: PFC0160w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="MAL3P2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Plasmodium falciparum 3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolate="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _type="genomic DNA"
                                                                                                                                (611 aa) fasta scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-9 and 13
                                                                                                                                                                                                                                                                Ank repeat; Pf finger domain,
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IFCCCLABILITY IN THE TREE FEWENTINE THAT THE PERCYCHANNANNANNET TO EXAMPLE THE TREE TRAINING THAT THE PERCENT TO EXAMPLE THE PERCENT THE PERCENT THE PERCENT TO EXAMPLE THE PERCENT THE P
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LYDVVNNYHRIYNCYTRLYINDDFLLINKTKEILGYQNVASHINNTTWNNMNIDNI
HNVNNINNYNMREHLKRIEKKNKINNYNNNNNDDELSTDTGDDMLSNNCEYNEE
SKYYKLVLIKKNTLKHLFNNOCTDINLFSFHARCLSNYNKLDENYSYLLINNYNLNNK
SEHLINISRKKNYTLDHTNNTYNNSNTNIITKNYSNNNHNNNNDNILSNDLYSYFNN
YLTKKIVENYSTYSLYIKECLLIIDILYILNTYGNLIYIKKOHENYYNIISN
IVQKKNEKRKKKSYKNIYDHSKENNRKQSNSIYSISFOKNNNINYINKRULNNLHGE
EIPDDSNSSSNISSSNNSSSNKSSHNSATSYDLFKMRKRNNLNYINKRKQLNNDLIY
FFPKYKLIIHFTLLNVNEQNNSNIEIAREILYLGIYIRKIQKFIEINKRSQSCNFTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWALL: Q962L5 (EMBL: AY003872) blast scores: B(): 0.0, score: 2249 43% id, and to Plasmodium falciparum thioredoxin-like redox-active protein fred SWALL: Q9NC62 thioredoxin-like redox-active protein fred SWALL: Q9NC62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mmnreklikllekenknrmniknvkfrdchcmfnnysQcyvnvk
nkyenndfwkyeniygndniikrsvqeesekkkwiednynkessleftypyryesnrn
ifliinseninlgnscyynndliyiihnnkryehmnlfkrtkkkkkkkkkrtketkr
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YYSSIENKNTNVEQLCIKNRYELVYILLKKWYLQNKICSKLKICKIYAPY PWFFALK
NLIVYENIAHSESIINKYHFYKSLIMITINFFQOELWCHLYFKSPGFYKENMFYNKNK
KIQSSKYKNSNPMYNGTFKTINAEYQLNNIEREIFQINKKLISTNFNTLTPINHDQALS
NKYNDILINLEYQKLSIYSQVSQERINSLDEDYRNAILYNQNERNICVTCNIIKEPRV
HHCARCFHCIVHQDHHCYWUNCIGIKNORCFYMFIFGIFVLLLYNYYYYYLYFHLFG
ATINYAPGSLVILCNPINVTLFAFITYLFARNTRTILTNVTFYEHYKKPNHITDKYNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.87% id in 197 aa, and to Rattus norvegicus small rec
sreC SWALL:Q9JKR5 (EMBL:AF228917) (366 aa) fasta scores
(): 8.4e-09, 27.95% id in 161 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRTLHMMKNDTFGSVTSMNDEKDYMKYNQDYHDKDDDDYDDEDDDDDDDDDDDDDD
YEDDDDDDYDDDEDNYNNSYDNSYDNGYNTKHNKKKINPMYNSTIFETSNMNFCVKDE
KRKKKEKQKNSIDKKNIIYSDDDSDNNYEHIFTHINSDLFFLSISNDHIBKENNLYIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similar to Plasmodium vivax pvlh14095 p pvlh14095W SWALL:Q962L5 (EMBL:AY003872) blast scores: E(): 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLNSINILHWACYCGFTELVKKLISFNCDIEKEDLVNNDT?IYYAIKNSNYEIVLLLI
KCFGISILFHKNRRRMSPFLTAICEFNEDKILEALHILELLYMNGVSLEEQNEHGQTA
                                                     LLRDKAYISMIQNTIKHYDKHFKNFFLLLTTHINNHPHNQYHNNNKYNNKNNYHKKIIQE
KFNFDKAYISMIQNTIKHYDKHFKNFFLLLTTYVNNNIDEYAHNFLIKLDYNFYYTNKY
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KLSYQNPTSFNNDINSBYVNDNFNDNLDDSNDTRQVTKENVNGTNYNNNVSKYNHMQT
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/product="hypothetical protein, conserved'
/protein_id="CAB38989.3"
/db_xref="G1:23477022"
/db_xref="SFTREMBL:097225"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.42% id in 175 aa"
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/product="binding protein, putative"
/protein_id="CAB38988.3"
/db_xref="G1:23477021"
/db_xref="SPTREMBL:097224"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="MAL3P2.2"
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CDS gene

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ACCESSION
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AC005506/c
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                    Plasmodium falciparum chromosome 12 PROGRESS ***, 4 unordered pieces. ACC005506
    AC005506.8
                                                                                     AC005506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                   AATACTTTAGACGCAACACAATTTATAGACGCGGAGGAAA 242
                                                                                                                                                                                                                                                                              TTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGCAACACAATTTATCGATAAATA
                                                                                                                                                                                                                                                                                                                                                               ACACATACATGTTCTTTTTTATACAAAAAATAATACAACACAATATTAATTGTGTTGTA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGCTGGTACAAGTGAAGCAGTTAAAAAATGGGTAAACAA 118663
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/gene="MAL3P2.3"
/note="synonym: PFC0170c"
complement(13855...15201)
/gene="MAL3P2.3"
/EC_number="2.3.1.-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Similarity to lipoamide acyltransferases. eg C.elegans lipoamide acyltransferase (MP.ZK65, 4) BIAST Score: 582, sum P(1) = 9.2e-57, 33 identity in 430 aa overlap; similarity to P. vivax PVIHI4105C, 59.908 identity (61.611 ungapped) in 434 aa overlap Pfam match to entry PF00198 2-oxoacid dh, 2-oxo acid dehydrogenases acyltransferase (catalytic domain), scoil 140.90, E-value 2.2e-38; Pfam match to entry PF00364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Revised: split original spliced gene PFC0165w into PFC0165w and PFC0166w, fasta; plasmodium falciparum; thioredoxin-like redox-active protein; freb; length 179 aa; id=100%; ungapped id=100%; E()=2.1e-69; 179 aa over1ap; query 1-179 aa; subject 1-179 aa; fasta; TR:AAF99466 (EMBL:AY003872); plasmodium vivax; pvlh4100; pvlh14100w; length 179 aa; id=65.92%; ungapped id=67.42%; E()=1.5e-40; 179 aa over1ap; query 1-177 aa; subject 1-177 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biotin_lipoyl, Biotin-requiring enzyme, score 46.20,
E-value 7.4e-10
Similar to Arabidopsis thaliana branched chain alpha-keto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:Q81224"
/translation="MACQVDNPPKTYPNDKTAEYEKYANYMNYLYYYQNNELKKIDSS
YFKDKYLGLFFGASWCKYCVTFIDSLNIFKKNFPNVEIIYIPFDRTYQEYQSFLKNTN
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NILNNNKOTIILSENPYLKEXNHIPFQNKNHDTPSPLHINNFNQDENNNISPLNYSKLK
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IIHPKTFQFNNRFFDLFRN"
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/protein_id="CAD49085.1"
/db_xref="G1:23477023"
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                                                                                   205429 bp
                                                            DNA linear clone 3D7, ***
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                                                               SEQUENCING
                                                                                   HTG 12-AUG-2000
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AUTHORS
TITLE
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AUTHORS
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Plasmodium falciparum (malaria parasite P. falciparum)

Plasmodium falciparum

Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 205429)

Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Tamaki,T.,
Kurdi,O.B., Conway,A.B. and Davis,R.W.

Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Aug 12, 2000 this sequence version replaced gi:8810449.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contidgs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-AUG-1998) Stanford Center, Stanford University, 855
                                                                                 complete sequence.
AE014846 AE014188
AE014846,1 GI:23496645
                    Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
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  Eukaryota;
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                                                                                                                                                                                                                                                                                                                      AATACTTTT
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/chromosome="12"
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/mol_type="genomic DNA"
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Alveolata; Apicomplexa;
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132469: gap of unknown length
192227: contig of 59758 bp in length
192427: gap of unknown length
192427: gap of unknown length
204064: gap of unknown length
204064: gap of unknown length
204064: gap of unknown length
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/note="Hindfam hit to PF00226, DnaJ domain, score 2e-39" /note="Hindfam hit to PF00226, DnaJ domain, score 2e-39" /codon start=1 /codon start=1 /product="heat shock protein DNaJ homologue Pfj4" /protein id="AAN36202.1" /db_xref="GI:23496646; /translation="MSRRVNYYEVIGVPQDADLTVIKKSYRTLAMKWHPDKNPNNKAE /translation="MSRRVNYYEVICTEDENWAADENDEFSNEHKNEGENUAQRIFE MFEGDSSPFGNDSFFSDVMGSSFVDKRRGRVPRSNDFPDNFFGSSFNDAQRIFE MFEGDSSPFGNDSFFSDVMGSSFVDKRRGRVPRSNDFPDNFFGSSFNVSFGSSFDNFM DGGSCFTSVETSTSNGGERKNRVVKTSTSKSTSIINGKRVTRIETVKTLPNGTVERTV TEREBDDRGNINIRGIPAHELRRNKR" 35003544 /rpt_type=tandem 38733905	330 780 . 1	/rpt type=tandem 2249 . 2282 /rpt type=tandem 2553 .2591 2553 .2591 /rpt type=tandem 2865 . 2909 /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem	/organism="plasmodium falciparum 3D7" /organism="plasmodium falciparum 3D7" /isolate="3D7" /isol	pain, A. Nene, Vertean, J.A., Ruth, M.S., Nene, Vertea, M., Allardya, A.B., I. Roos, D.S., Subramanian, Hoffman, S.L., Subramanian, Hoffman, S.L., Subramanian, Hoffman, S.L., Conwaley, D., Tamakision, California
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KVDMMNILS YDNHAII YNNYYDYGDLYNKVVRAVSSTNANI DDEERKEKKKEDISKT
ELYYNKKKRRSMMDLLMECTEEI FTEMNININENFTMEENKMLMVTLQSRYGYGSDLRE
TSIAMSRLPESNYLDIDMCFXYGSNNYILKNIKYYDKIKKONDYTLQSRYGYGSDLRE
TSIAMSRLPESNYLDIDMCFXYGSNNYILKNIKYYDKIKKUNDYTLQSRYGYGSDLRE
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KYVIVALPLGCLIENNDKKRKKKTKTCKFEPELHPLKLRALQNYKMONHIKIILFEYDN
KYVIVALPLGCLIENNDKKRKKKTLYTITTAKQDDNFSFGSYAPYNNODINIYLRASPHPINN
FTWPFDSLQINCIDQKFGFLNLHAYGKIGCILVHCFPPMSCTYGYIKKEHYIINDFXKYKTDVYIFPQNKC
PFTNIPLDFIKKKFLGFYITDGSDEALTDYESGSYAPYNNODINITLTLRSPHPINN
RVVFCGEYLSKSYFGCVUGANOTIGIRAAEDIAHIGLHLKNNDTKKYKTDVYIFPQNKC
PFTNIPLPFIKKKFLGFYITDGSDEALTDYESGSNAWTNNDLIYLLSTLLDIN
NTNSNTSSNNNNTNKTNYTONNI DISVKKKYKGSYILLELHSKDSENDSNNNDANICTIL
NLYMKTKYTDDJALKCSSYKKEN KSNTSSNNNSLINGSNLX
NLYMKTKTONTONNIKADHNOVYNDKYTNOKYNNSLINGENDSNNNDANICTIL
TTYNNKKTDOJTHYDRIKGSDLXNNDKANDANICTIL
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KELFLKIQAMKHILFNUNNFQSLQDMVYLSQALHKUDHIVSHNHMUDVDRKKAYEQ
NTDIINEDDKEISYFHEKMEEVNINKIKKLSLALIKSNMVGNNUDDDNNNNGHIÇKS
NISTDBIDINKIINASKTKNNNITNKKDVMIQTNLNIYNNIDLQNKIKNIYINNRKIC
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SEDQQKSNNNYVSDDTNEKDSDYFYNNDILKEDKQINNNILIDDTYHKEILFNNNHVK
NIKPNENNIIRNENFEASVLYNNKDDMKLENGENGKNAENGKNEENGENGKNAENGKN
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QDDENKTGDKNKISGCONGIYRYLNSKKNISCNSOIYSYSSDEDYFYSRIKNR
KIKLRNMLFWHIKNNIDIRNYFKIYNKEKKNNILNFFKSLDEDIHFYNNLSDSCYPT
SSVLYPKNNCTNKSNKLLKILSFNKDTRRRREYDKSVTQLAEKLKPRVSLVCGKDNWE
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KVKTKKKISLFGIVKPEDIIKRGINNVYHNIEDNGKLYTDVLIGAGISGLAASYYLN
KVATAKKISLFGIVKPEDIIRROJERRIINKYLPETVVDLGANYLHCCONADLTUNK
KCNAKFIVIEGERNIGGRAFSTILPERIINKYLPETVVDLGANYLHCCONADLTUNK
KGKTKHEFANCTEFNNEKSMRKEDDIDYEDNFINNMKKKKTKKKKYKVIVKKRKYNYN
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STVNTKVVIQLLCDYIYYLIFCKHDILCYKCMNGGELNMCDSYNCNNSWHTYCLSSSE
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IRKRLDLLKAHLSRSVA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
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Plagiochasma rupestre
Plagiochasma rupestre
Plagiochasma rupestre
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Marchantiophyta; Marchantiopsida; Marchantiidae; Marchantiales;
                                                                                      Clavija spinosa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Ericales; Theophrastaceae; Clavija.
                                                                                                                                                                                                                                   AF402569 1018 bp DNA linear Clavija spinosa ribosomal protein L16 (rpl16) gene, sequence; chloroplast gene for chloroplast product. AF402569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (18-MOV-1999) Capesius I., Botanisches Institut,
Universitaet Heidelberg, Im Neuenheimer Feld 360, 69120 Heidelberg,
        Phylogenetic Relationships in Primula L. (Primulaceae) based on Noncoding Chlorop
                                                            Mast, A.R., Kelso, S., Richards, A.J., Lang, D.J., Feller, D.M.S.
                                                                                                                                                                           chloroplast Clavija spinosa
                                                                                                                                                                                                                   AF402569.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capesius, I. and Bloecher, R. A molecular approach to bryophyte systematics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marchantiineae; Aytoniaceae; Plagiochasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTTTAACGCAACACAATTTATCGATAAATAATACTTT
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ilarity 58.1%;
Conservative
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/product="small ribosomal protein 4"
/product="small ribosomal protein 4"
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/db_xref="goA:Q9M4C3"
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PTIPGARQLVHHQHILLINNITUDIPSYNCKPKDIITINDRUGSGSIITKNLNFFQKQK
IPNHLTFDLIQFKGLINQIVDRECIYLKINELLVVEYYSRQV"
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/mol_type="genomic DNA"
/db_xref="taxon:53031"
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Pred. No. 8.
Noncoding Chloroplast
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Mismatches
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AC115683/c
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Best Local
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29150 bp DNA linear INV 12
Dictyostelium discoideum chromosome 2 map
complement(6135149-6105997) strain AX4, complete sequence.
Direct Submission
Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 29150)
Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-JUL-2001) Institute for Systematic Botany, of Zurich, Zollikerstrasse 107, Zurich 8008, Switzerland Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mast, A.R., Kelso, S., Richards, A.J., Lang, D.J., Feller, D.M.S.
                                                                                                                                                         Submitted (22-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 29150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dictyostelium discoideum Dictyostelium discoideum
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2 (bases 1 to
                                                                      Biotechnology, Beutenberstr. 4 (bases 1 to 29150)
                                                                                                                                              Baumgart
                                                                                                                                                                                                                                                                                                                       Sequence and analysis of Nature 418 (6893), 79-85
                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                    Baumgart,
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                                                                                                                                                                                                                                                   The Dictyostelium Genome Sequencing Consortium 2 (bases 1 to 29150)
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                                                                                   (04-MAR-2003) Genome Analysis, Institute of Molecular logy, Beutenberstr. 11, Jena 07745, Germany
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db_xref="taxon:175025"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Clavija spinosa"
/organelle="plastid:chloroplast"
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Pred. No.
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and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
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EEVVUNKQRESFENNYNKERKATVYNLSERYSSYTSIYLMAMKEGDIDTMERLDKSWNP
VIRLDVSREHYFQLPKEKEVLMKVWDYLLEHSFKQIGNNYEILMEFFSSVTDVISPLD
LKISNLEDETMKRLGLILFNYLIINNLAVFQLLLNSFDNFNFLSEIVVEVNNTLLNEKK
ILFGSGGKIMQIDNKYINQLIKSIEMAVEKYNKFISEPIENGVESFSIILNHLYDQLI
RIKGISVDQLDYIRSIIPDQLLAFKCELYRTFFYLNIRGKLTKYILTRENISLYTEG
TPNHYAMHSGLYNIHSNIGPSALDLRKYLKLDIFTYDYIIGRENSSSGGGADDNNNY
NNNNNNNTRKFINQFDTILKELIKQLSFDICTNVSNRDSIVDGKDFNYSLNADLR
FSLDIGRKDLFWELLDWIEQYMIKNENLMKYQVYQFNSPYESLLFTGAIFLNVKIIKL
PSPKTXTTKTIESRILKIDNFEKPIPNESUKIGWNTDKLIKPEKPIKLLINGFYQN
DVIBSICKVMKVNELLDWIEQYMIKNENLMKYQVYQFNSPYESLLFTGAIFLNNKIIKT
PSTFSEVNKNYSQYLEYMLEKRYFEFPLVLLNSFVVYLCDQDNISDYNQFIQNNSLQI
RNKVMKKTIIILIENGLEXPLEKRYFEFPLVLLNSFVVYLCDQDNISDYNQFIQNNSLQI
RNKVMKKTIIILIENGLEXPLEKRYFEFPLVLLNSFVVYLCDQDNISDYNQFIQNNSLQI
RNKVMKKTIIILIENGLEXPLEKRYFEFPLVLLNSFVYLCDQDNISDYNQFIQNNSLQI
RNKVMKKTIIILIKFYYKVGNFNEDYSIIIYFTFEFAIKCLNLETIKELVNLESINFK
SDTLRMKNIHIIKYYYKVGNFNEDYSIIIYFTFEFAIKCLNLETIKELVNLESPSTRKKL
NYGIKLISEEFKKAARRKTPKTTIABYIFSPSNBLYSIPTLLNNKOQOBESTNKKL
NYGIKLISEEFKKAARRKTPKTTIABYIFSPAIKGLNNGCOBESTNKTL
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Location/Qualifiers
                                                                                                                                               RDDIMSFLINNYNIKLNGFPTFSKADNOHSQYLECKSIFENHFEKVKNISKLKLEWCE SRDLOFPLVLLNAFVVYLCNDRNFSTYSBFIQNDNLEIRNKAIKEIIKKLKYHYEDDE EEYNLDENFASIIKNQNHKVSIIQPIIEQPDTQLYFKSVLDHVTLKIKKERKICGA" complement (join 19122. . 12850,13367. . 13503,13670. . 13805); /note="GeneID exon scores (in order of location ranges): 182.36, 4.06, 2.27 - GSCU_ID dd_00733"
                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein"
/protein_id="AAL92693.2"
/db_xref="GI:28828562"
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complement(join(979. .3698,4376. .4909,4970. .8456))
/note="GeneID exon scores (in order of location ranges):
160.08, 15.36, 208.53 - GSCU_ID dd_00748"
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LKSSILLKSFMELDIVKGEFKNNNVNSFLKMYHPYERLKVNIQIILKYGTPSLDTKET
KBILDKIDNIDQKDSNHLLKLQEFAALHFPNQKNFYFYYSKKYGGKIKQLGKVPPKTP
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KFKRKSLSLAAHRKTIKTSITEYIFNNPSLYSIPPPLSLINNQKQQTQSKNKRLKLSE
ILLSNFNNKNDNTTSEEDENDGVEDEDVQENEDDGAEDEGDEDEGEDDGDEEDDEEED
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RCKfkytyslQimirngllplikdkikhGdhieidhnsikilflklsktQpiQpynQk
EitlfnisnnnnnnnnnnnnnnnnkykdedylbiielfmkhrrdQfeitdlikdkok
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NEDIDTQQQQQQQQQQQQQQQQQQQQQQQQQQQXQQQKQQIQLLQVKNVNKRREFL
NGFDIPLTFNDSSSSLKTLLYLSAMREGDVDKIKMYDGAFSARFRLDVSGFHYFKLPK
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db_xref="GI:28828563"
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/trānslation="MTEKTEILFWKVFKNDFIFKEIFNQIHNNQWIEYDNPNKYSVYN RYEDYLEIIELLIKHRRDEFEITDLINIATNKNSPDVIRLLVNEPYSMTEKTEILFWK

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                            AATACTTTTAGACGCAACACACTTTAT 228
                                                                                 TTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGCAACACAATTTATCGATAAATA
                                                       20.8%; Score 51.8; Dilarity 53.1%; Pred. No. 5.6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           /note="GeneID exon scores (in order of location ranges):
234.39 - GSCJ_ID dd_03403"
                                                                                                                                                                                                                                                                                                                                                                  KEDRKNDEINSPFIENNKNPFIESFIHGDIKTCDIILKYYPNQFKITKDSITETLKME
NIHIIKYYYKYDNCKNLINNFKNDNNLLKHLKNELSKHPIYKYHLTWL"
                                                                                                                                                                                                                                                                                                                                                      complement(24533. .28629)
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Search completed: February 28, Job time: 1257.82 secs 2004, 07:53:31

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Abl33519 Human imm
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Listing first 45 summaries
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  misc_binding
30-JUN-2001; 2001US-00895435
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TnpI recognised target; TRT''; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B. thuringiensis InpI recognition target sequence TRT''.
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174..193
/*tag= e
/bound_moiety= "
176..227
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/rpt_type=
112, .125
/*tag= d
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/bound_moiety= '
112...143
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/rpt_type=
176. .191
/*tag= g
209. .229
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/note= "Tn4430 left IR"
112. .145
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Result

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Minimum Maximum

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Searched:

Total number of

Scoring table: Sequence:

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Database

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RESULT 2
ABZ75335
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AC ABZ7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EUMO-)
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  repeat_unit
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                                                                                                                                                               Bacillus thuringiensis
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                                                                                                                                                                                                                                                                                                                                                                                                        ABZ75335;
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recognised target; TRT''; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGTACCGCCAGCATTTCGGAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 103 A; 38
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                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                              Location/Qualifiers 37. .59
     /rpt_type= DIRECT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
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Best Local :
                                                                                                                                                                                                                                                                                                                                             molecule comprising Inpl recombination substrates. The composition may have a use in gene therapy, and as a vaccine. The recombinase Inpl and the recombination substrates IRF or IRF' sequences are useful for genetic engineering. The kits are useful for Inpl-mediated genetic recombination. The Inpl-mediated site-specific recombination is useful for deleting or inserting DNA sequences to modulate gene expression, integrating new nucleotide sequences into a DNA molecule, such as an episome or genomic DNA, for gene therapy, or for producing food-grade genetically modified organisms. The present sequence represents the Inpl recognised target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A composition comprising recombinase TnpI and the recombination substrate TRT or TRT' sequences, useful for genetic engineering, TnpI-mediated genetic recombination, or for gene therapy.
                                                                                                                                                                                                                                                                                                          Sequence 244 BP; 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Fig 1A; 58pp; English.
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241
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UNIV CATHOLIQUE LOUVAIN.
                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                       GGTACCGCCAGCATTTCGGAAAAAACCACGCTAAGAAATCAGAGTTAAAAAATCAGAA
 TCAC
                          TCAC
                                                  CACAATTTATCGATAAATAATACTTTAGACGCAACACAATTTATAGACGCGGAGGAAA
                                                                        CACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAGACGCGGAGGAAA
                                                                                                  CAATATTAATTGT
                                                                                                                              CAATATTAATTGTGTTGTATTAGGTGTTATAATAATATAAATCTAGGGGTTTAACGCAA
                                                                                                                                                      AATATATCATTATTCCTTGACACATACATGTTCTTTTTTTATACAAAAAATAATACAACA
                                                                                                                                                                                                         GGTACCGCCAGCATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAGAA
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang
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244
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111. .142
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175. .211
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                                                                                                     |GTTGTATTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGCAA
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Pred. No.
                                                                                                                                                                                                                                                                                                            33 G;
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                                                                                                                                                                                                                                                                                                            T; 0 U; 0
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7.7e-40;
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RESULT

182 120 122

180

240 242 62

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30

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ABZ75336 standard;
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                                                                                                               Query Match
Best Local
                                                                                                   Matches 118;
                                                                                                                                                                                     The invention relates to a novel composition comprising an isolated DNA molecule comprising TmpI recombination substrates. The composition may have a use in gene therapy, and as a vaccine. The recombinate TmpI and the recombination substrates TRT or TRT' sequences are useful for genetic engineering. The kits are useful for TmpI-mediated genetic recombination: The TmpI-mediated site-specific recombination is useful for deleting or inserting DNA sequences to modulate gene expression, integrating new nucleotide sequences into a DNA molecule, such as an episone or genomic DNA, for gene therapy, or for producing food-grade genetically modified organisms. The present sequence represents the TmpI recognised target
                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B. thuringiensis InpI recognition target sequence
                                                                                                                                                                                                                                                                                                                                                        A composition comprising recombinase TnpI and the recombination substrate TRT or TRT' sequences, useful for genetic engineering, TnpI-mediated genetic recombination, or for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Stewart FA,
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                                                                                                                                                   Sequence 118 BP; 49 A; 14 C; 15 G; 40 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                    Claim
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                        173
                                                                         113
                                                                                                                                                                                                                                                                                                                                 6; Page 55; 58pp; English.
61
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UNIV CATHOLIQUE LOUVAIN.
                                                                                                               Similarity
                                                                TTTAACGCAACAATTTATCGATAAATAATACTTTTAGACGCAACACAATTTATAG
                       TTTAACGCAACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAG 230
                                                 TAATACAACACAATATTAATTGTGTTGTATTAGGTGTTATAAAAAATATAAATCTAGGGG
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang Y,
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k; Pred. No. 9.5
0; Mismatches
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                                                                                                               9.5e-15;
                                                                                                                           DB 7;
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                                                                                                                       Length 118;
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118
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173

TTTAACGCAACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTAT 228

Best Loc Matches Query Match

Similarity

45.98;

Conservative

0

Score 114.4; DB Pred. No. 5e-14; O; Mismatches

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7;

Length Indels

116; <u>.</u>

Gaps

9

Sequence 116 BP; 47 A; 14 C; 14 G;

41 T; 0

U; 0 Other;

functional variant TRT'

The invention relates to a novel composition comprising an isolated DNA molecule comprising TmpI recombination substrates. The composition may have a use in gene therapy, and as a vaccine. The recombinate TmpI and the recombination substrates TRT or TRT' sequences are useful for genetic engineering. The kits are useful for TmpI-mediated genetic recombination. The TmpI-mediated site-specific recombination is useful for deleting or inserting DNA sequences to modulate gene expression, integrating new nucleotide sequences into a DNA molecule, such as an episceme or genomic DNA, for gene therapy, or for producing food-grade genetically modified organisms. The present sequence represents a TmpI recognised target (TRT)

Disclosure; Page 12; 58pp; English.

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A composition comprising recombinase TnpI and the recombination substrate TRT or TRT' sequences, useful for genetic engineering, TnpI-mediated genetic recombination, or for gene therapy.
                                                                                                                                                                                                                                                                                                                 Key
repeat_region
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                                                                                                                                                                                                                                                                                                                                                                             B. thuringiensis TnpI recognition target TRT'
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                                                                                                                                                                                                                                                                                                                                                      TnpI; gene therapy; recombinase; 'I
TnpI recognised target; TRT''; ds.
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                                                                                                                                                                                                                                                                                                                                                               gene therapy; recombinase; TRT; TRT'; genetic engineering;
                                                                                                                                                          Zhang Y,
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                                                                                                                                                                                                                                                                                                                                                                               functional variant
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RESULT 5 ABZ75340

ABZ75340

standard;

DNA;

116

ВÞ

06-MAY-2003 ABZ75340;

(first entry)

Bacillus thuringiensis

gene therapy; recombinase;
recognised target; TRT''; di

gg.

TRT; TRT'; genetic engineering;

repeat\_region

\*tag=

type=

INVERTED

Location/Qualifiers

B. thuringiensis InpI recognition target TRT' functional variant

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61

TTTAACGCAACAATTTATCGATAAATAAATACTTTTAGACGCAACAATTTAT 116

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                                                                                           Query Match
Best Local Sim
Matches 115;
                                                                                                                         molecule comprising TnpI recombination substrates. The composition may have a use in gene therapy, and as a vaccine. The recombinase TnpI and the recombination substrates TnT or TnT' sequences are useful for genetic engineering. The kits are useful for TnpI-mediated genetic recombination. The TnpI-mediated site-specific recombination is useful for deleting or inserting DNA sequences to modulate gene expression, integrating new nucleotide sequences into a DNA molecule, such as an episome or genomic DNA, for gene therapy, or for producing food-grade genetically modified organisms. The present sequence represents a TnpI recognised target (TRT)
                                                                                                                                                                                                                                                                             A composition comprising recombinase TnpI and the recombination substrate TRT or TRT' sequences, useful for genetic engineering, TnpI-mediated genetic recombination, or for gene therapy.
                                                                                                                                                                                                                                                                                                                                                     Stewart FA,
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                                                                                                                                                                                                                                                       Disclosure; Page 12; 58pp; English.
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                                                                                         Sequence 116 BP; 47 A; 14 C; 14 G; 41 T; 0 U; 0 Other;
                                                                                                                                                                                                                                  The invention relates to a novel composition comprising an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2003
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                                                                                                                 functional variant
                     113
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UNIV
                                                        Similarity
                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                           MOLECULAR BIOLOGY LAB CATHOLIQUE LOUVAIN.
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65. .11
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                                                     45.9%;
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                                            0
                                                        Score 114.4;
Pred. No. 5e
                                            Mismatches
                                                     5e-14;
                                                                  DB 7;
                                            1;
                                                                  Length 116;
                                            Indels
                                           0;
                                           Gaps
                                                                                                                                                                                                                                    DNA
60
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Query Match Best Local S Matches 64

Similarity

64;

Conservative

0

Score 64; DB Pred. No. 0.00 0; Mismatches

Length 116

0,

Gaps

172

Sequence 116

B₽;

27

A; 11 C; 25.7%;

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21 T; 0 U; 52 Other;

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RESULT 6
ABZ75342
ID ABZ7
The invention relates to a novel composition comprising an isolated DNA molecule comprising TmpI recombination substrates. The composition may have a use in gene therapy, and as a vaccine. The recombinate TmpI and the recombination substrates TRT or TRT' sequences are useful for genetic engineering. The kits are useful for TmpI-mediated genetic recombination. The TmpI-mediated site-specific recombination is useful for deletting or inserting DNA sequences to modulate gene expression, integrating new nuclectide sequences into a DNA molecule, such as an episome or genomic DNA, for gene therapy, or for producing food-grade genetically modified organisms. The present sequence represents a TmpI recognised target (TRT) functional variant TRT'
                                                                                                                                                                                                                                                                                                                                     A composition comprising recombinase TnpI and the recombination substrate TRT or TRT' sequences, useful for genetic engineering, TnpI-mediated genetic recombination, or for gene therapy.
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   Query Match
Best Local S
Matches 82
                                                                                The invention relates to a novel composition comprising an isolated DNA molecule comprising ThpI recombination substrates. The composition may have a use in gene therapy, and as a vaccine. The recombinase ThpI and the recombination substrates TRT or TRT' sequences are useful for genetic engineering. The kits are useful for TnpI-mediated genetic recombination. The ThpI-mediated site-specific recombination is useful for deleting or inserting DNA sequences to modulate gene expression, integrating new nucleotide sequences into a DNA molecule, such as an episome or genomic DNA, for gene therapy, or for producing food-grade genetically modified organisms. The present sequence represents a TnpI recognised target (TRT)
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Local s. 82;
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                                                                                                                                                                                                                                             composition comprising recombinase Tnpl and the recombination substrate RT or TRT' sequences, useful for genetic engineering, Tnpl-mediated enetic recombination, or for gene therapy.
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82; Conservative
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UNIV CATHOLIQUE LOUVAIN.
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CC of genes associated with development selected from 87 genes listed in the Cs specification such as ACCPN, ADRN, or APD1 and comprising one of 350 CC useful for the diagnosis or their complements. The invention is CC development genes, in particular disease related to homeobox containing CC genes (HOX), like diabetes, concer, apoptosis related diseases, syndromes CC associated with congenital heart disease, epilepsy, diseases related to fistone deacetylation, Currarino syndrome, diseases related to CC histone deacetylation, Currarino syndrome, diseases related with the CC development of the brain and limb girdle muscular dystrophy and dwarfism. CC Oligomers specific to each of the genes are useful for detecting the CC methylation state of all CpG dinucleotides within the 350 sequences or CC (II) and their complementary sequences, as primer oligonucleotides for CC the amplification of the 350 sequences, (II) and/or their complements and CC as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs). Note: The sequence data for this CC patent did not form part of the printed specification but is based on CC sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a nucleic acid (I) comprising a sequence a least 18 bases in length of a segment of chemically pretreated DNA of genes associated with development selected from 87 genes listed
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence associated with pretreated DNA of genes associated with
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                                                                    o;
                                                                                                                                                                     142
                                                                                                                                   687 AACTAAAAACCAAACCAATACCACCTTTACTAAAACTCAAAACCTATATATTTCTCTTA 628
                                                                                                                                                                                                       568
                                                                                                                                                                                                                                      143 TAGGIGITATAATAATAAATCIAGGGTTTAACGCAACACAATTTATCGATAAATAA 202
                                                                                                                                                                                                                                                                        508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               blood protein disorder; agammaglobulinaemia; dysgammaglobulinaemia; ataxia telangiectasia; common variable immunodeficiency; lymphopenia; thrombocytopenia; haemoglobinuria; Addison's disease; Grave's disease; haemolytic anaemia; multiple solerosis; rheumatoid arthritis; lupus; endometriosis; autoimmune thyroiditis; anabylaxis; hypersensitivity; autoimmune pulmonary inflammation; organ rejection; inflammation; CLASP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising an amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polypoptide (I) comprising an amir acid sequence that has 90 % sequence identity to one of the human cadherin-like asymmetry protein(s) (CIASP)-2 (hCLASP-2A, 2B, 2C, 2E) sequences (PS). (I) is useful for identifying a compound or agent that binds CLASP-2 polypeptide. An antibody (II) to (I) is useful for detecting a CLASP-2 polypeptide in a sample. (II) is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human cadherin-like asymmetry protein(s) (CLASP)-2 for modulating immune response, and for treating multiple sclerosis, rheumatoid arthritis, endometriosis, lupus, autoimmune thyroiditis, septic shock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; autoimmune disease; haematopoietic disorder; Digeorge syndrome;
                                                                                                                                                                                                                                                                      83 CACATACATGTTCTTTTTTTATACAAAAATAATACAACACAATATTAATTGTGTAT
                                                                                                                                                                                                     23 AAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAGAAAATATATCATTATTCCTTGA
                                                                    Gaps
                                                                    ö
   Seguence 6550 BP; 1589 A; 235 C; 1752 G; 2974 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cadherin-like asymmetry protein-2 (CLASP-2) genomic DNA
                            20.2%; Score 50.2; DB 6; Length 6550; llarity 53.9%; Pred. No. 0.34; Conservative 0; Mismatches 88; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 12B; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             ABK85018 standard; DNA; 43545 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-2001; 2001WO-US032202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-OCT-2000; 2000US-00687837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ARBO-) ARBOR VITA CORP. (GARM/) GARMAN J D. (CAND/) CANDIA A F.
                                                                                                                                                                                                                                                                                                          203 ATACTTTAGA 213
                                                                                                                                                                                                                                                                                                                                           507 ATAATTTAATA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-416861/44.
                                                al Similarity
103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200231117-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK85018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; ds.
                                   Query Match
                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lu PS;
                                                                                                                                                                                                                                                                                                                                                                                                               ABK85018/c
                                                                    Matches
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RESULT

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inhibiting a immune response in a subject. A pharmaceutical composition comprising a nucleic acid encoding (1), or (II) is useful for preventing or treating a CLASP-2 mediated disease e.g. an autoimmune disease, where the autoimmune disease is caused or exacerbated by increased activity of TH1 cells. CLASP-2 polymucleotides are useful as probes or primers for checation or inhibition) of CLASP-2 expression (e.g., antisense or riboxinon of CLASP-2 expression (e.g., antisense or cholymucleotides can express CLASP-2 polypeptides, produce anti-CLASP-2 polymucleotides can be used in diagnostics (e.g., as probes for CLASP-2 expression), as a lymphocyte marker and for therapeutic C purposes. CLASP-2 polymucleotides can be used in diagnostics (e.g., as probes for CLASP-2 expression), as a lymphocyte marker and for therapeutic collymucleotides can construct transapenic and knockout animals, e.g., for screening of CLASP-2 agonists and antagonists. CLASP-2 polymucleotides can construct transapenic and knockout animals, e.g., for screening of CLASP-2 agonists and antagonists. CLASP-2 polymucleotides can treat deficiencies or disorders of hematopoietic cells and can treat deficiencies or disorders of the immune system, by activating or inhibiting the activation, differentiation of immune cells and can treat or detect deficiencies or disorders can increase differentiation and proliferation of haematopoietic cells. CLASP-2 polympetides or centation of haematopoietic cells including the pluripotent stem cells to treat those conformed disorders (e.g., agammaglobulinaemia, exaxia telangiectasia, common variable conformed disorders diseases, multiple sclenosis, hymphopenia, thrombocytopenia, or detect autoimmune diseases, e.g., Addison's disease, haemolytic anaemia, cendence disorders disease, multiple sclenosis, autoimmune thyroiditis, and autoimmune pulmonary conformation or conformation or classes, auticinamia, autoimmune diseases, multiple sclenosis, and autoimmune pulmonary conformation or classes, auticinamia, auticinamia, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypersensitivity to an antigenic molecules, organ rejection or graft-versus-host disease (GVHD) and inflammation. ABK84922-ABK85018 represent cadherin-like asymmetry protein (CLASP) coding sequences and PCR primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7809 AATAAAATAAAATAAAAAAGTAAATAATTTATCTTTCTTCCATAAGATAATTTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 ITTITITATACAAAAAAAAAAAACACAATATTAATTGTGTTGTATAAGGTGTTATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AmEPV; gene therapy; viral vector; chromosome mapping; gene mapping; genetic deficiency disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43545 BP; 12383 A; 8378 C; 8983 G; 13801 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203/c
ABL56203 standard; DNA; 32392 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amsacta moorei entomopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 61.5%;
Matches 80; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7689 CAATATATAT 7680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 AAATATAAAT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AmEPV genome fragment#5
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10-AUG-2001; 2001WO-US025287.

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The invention relates to a recombinant entomopox virus (BPV) vector, comprising a polynucleotide encoding a protein operably linked with a heteratologous promoters sequence. The invention also concerns methods for providing gene therapy for genetic deficiency disorders. Vectors of the invention are useful for delivering a polynucleotide encoding a protein to a vertebrate cell preferably a mammalian cell, such as a miman cell.

The vector is introduced into the vertebrate cell by infection in a viral particle, or by transfection, transduction, or injection either in viron or in vivo. The vector is useful for the delivery and expression of biologically useful proteins in gene therapy protocols, and for biologically useful proteins in gene therapy protocols, and for collivering large DNA segments for engineering of vertebrate cells.

Polynucleotides of the invention have applications in techniques such as their use as insertion sites for foreign genes of interest, hybridisation production of sense or antisense mucleic acides, vectors of the invention provide for stable integration and expression of hererologous DNA in host calls, and are adapted for accepting large hererologous polynucleotide colls, and are adapted for accepting large hererologous polynucleotide colls, and are adapted for accepting large hererologous polynucleotide expressed in a stable fraction. The current sequence represents a morner fragment of the genue of the genus B entomopoxvirus from amesacta moorei
                                                                                                                                                                                                                                                                            Novel recombinant entomopox virus vector useful for delivering polynucleotide encoding protein to vertebrate cell, comprises polynucleotide encoding protein operably linked with heterologous
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 226-242; 326pp; English.
                                                10-AUG-2000; 2000US-0224479P.
14-SEP-2000; 2000US-00662254.
                                                                                                                                                                               Bawden AL;
                                                                                                                         UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                           WPI; 2002-227161/28.
                                                                                                                                                                                                                                                                                                                                                             promoter sequence
                                                                                                                                                                          Li Y,
                                                                                                                                                                             Moyer RW,
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Gaps Sequence 32392 BP; 13748 A; 2577 C; 2550 G; 13517 T; 0 U; 0 Other; . 0 Score 49.8; DB 6; Length 32392; Pred. No. 0.43; 0; Mismatches 97; Indels 0; 20.0%; Local Similarity 52.7%; les 108; Conservative Query Match Best Loca Matches

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29772 29771 CAGTACAATATATATATATTATTOTTCTTCTACAAACAACACATAGAATTAGATTAAT 29712 29831 AAATACTTTTACAATCIGTATTATAATAATCTTTAATCCAAATATATTTATTATTTIGTT 셤 ò 8 8

à

ABL55643; RESULT 11 ABL55643 SEXEXEX

ABL55643 standard; DNA; 50000

(first entry) 01-JUL-2002

AmEPV genome fragment#1.

gene therapy; viral vector; chromosome mapping; gene mapping; genetic deficiency disorder, ds. 

entomopoxvirus Amsacta moorei

WO200212526-A2

14-FEB-2002

10-AUG-2001; 2001WO-US025287

2000US-0224479P. 2000US-00662254. 10-AUG-2000; 14-SEP-2000;

(UYFL ) UNIV FLORIDA

Moyer RW, Li Y, Bawden AL;

WPI; 2002-227161/28

Novel recombinant entomopox virus vector useful for delivering polynucleotide encoding protein to vertebrate cell, comprises polynucleotide encoding protein operably linked with heterologous promoter sequence.

Disclosure; Page 125-150; 326pp; English

The invention relates to a recombinant entomopox virus (EPV) vector, comprising a polymucleotide encoding a protein operably linked with a heterologous promoter sequence. The invention also concerns methods for providing gene therapy for genetic deficiency disorders. Vectors of the invention are useful for delivering a polymucleotide encoding a protein to a vertebrate cell preferably a mammalian cell, such as a human cell.

The vector is introduced into the vertebrate cell by infection in a viral particle, or by transfection, transduction, or injection either in vitrol particle, or by transfection, transduction, or injection either in vitrol or in vivo. The vector is useful for the delivery and expression of biologically useful proteins in gene therapy protocols, and for delivering large DNA segments for engineering of vertebrate cells. Polymucleotides of the invention have applications in techniques such as probes, for chromosome and gene mapping, in PCR technologies, and in the probes, for chromosome and gene mapping, in PCR technologies, and in the probes, for chromosome and gene mapping, in PCR technologies, may in hor probes. provide for stable integration and expression of heterologous DNA in host cells, and are adapted for accepting large heterologous polynucleotide inserts which can be delivered in an infected or transformed cell and ragment of the genome of the genus B entomopoxvirus from amsacta moorei expressed in a stable fraction. The current sequence represents

Sequence 50000 BP; 19857 A; 4373 C; 4222 G; 21548 T; 0 U; 0 Other;

ô Gaps ô ilarity 52.7%; Conservative Best Local Similarity
Matches 108; Conserv Query Match

2621 143 24 AAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAGAAAATATATTCATTATTCCTTGAC 84 ACATACATGITCTTTTTTATACAAAAATAATACAACACAATATTAAATTGIGTTGTATT 셤 à g à

2681 음

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racacarraaaggarraraargrar 2706 204 TACTTTAGACGCAACACAATTTAT

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12 RESULT

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1357/c
ABL32357 standard; DNA; 9642 BP.
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2002,
                                                                                                                    26-MAR-2002
                                                                                 ABL32357;
      RESULT 13
ABL32357/
                                                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid retukaemia, Alzheimer's disease, Alz, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 ATTAATTGTGTTGTATTAGGTGTTATAAATATAAATCTAGGGGTTTAACGCAACACA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCATTATTCCTTGACACATACATGTTCTTTTTTTATACAAAAATAATACAACAAT 126
                                                                                                                                                                                              antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Albieimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 CCGCCAGCATTTCGGAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAGAAAATA
                                                                                                                                                                               Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 9905 BP; 3133 A; 75 C; 1920 G; 4777 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 19.7%; Score 49; DB 6; Length 9905; Local Similarity 51.1%; Pred. No. 0.6; Los 115; Conservative 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 ATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAGA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 35; 32pp + Sequence Listing; German.
                                                                                                                                        Human immune system associated gene SEQ ID NO: 35.
ABL32062/c

XX
AC
ABL32062;
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Buman immune system disease; cyto
And antiarteriosclerotic; antianaenic;
Antiarteriosclerotic; antianaenic;
Antiarteriosclerotic; antianaenic;
Antiartelmanator; cancer; eye dise
Acute myeloid leukaemia; Albahamator;
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Antiartelmanator; cancer; eye dise
Acute myeloid leukaemia; Albahamator;
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Acute myeloid leukaemia; Albahamator;
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MO20200928-A2.
XX
A 03-JAN-2002;
XX
C 01-SEP-2000; 2000DE-01033529.
PR
A C-JUN-2001; 2001WO-EP007537.
XX
MU-SEP-2000; 2000DE-01043826.
XX
C 01-SEP-2000; 2000DE-01043826.
XX
C Olek A, Piepenbrock C, Berlin K;
XX
Mucleic acid comprising fragment C
diagnosis and treatment of disease
PT
Methylation.
XX
C The present invention provides a recomb and arterioscle:
C Including eye diseases such as retomb and recomb and arteriod arthritis, psoriasis and diseases. The present sequence is
XX
C Sequence 9905 BP; 3133 A; 75 C; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AnDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                    antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eq disease; anti-inflammatory; cancer; averiantial; alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AGCATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAGAAAAATATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 ITATICCIIGACACAIACAIGIICIIIITIITAIACAAAAAIAAIACAACACAAIAAIIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 IIGIGIIGIATIAGGIGITATAATATATAAATICTAGGGGITTAACGCAACAATITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9642 BP; 2381 A; 88 C; 2349 G; 4824 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 330; 32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 TCGATAAATAATACTTTTAGACGCAACACAATTTATAGA 231
                                                                 Human immune system associated gene SEQ ID NO: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin K;
                                                                                                                                       system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
(first entry)
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Best Local Similarity 51.4'
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
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(first entry)

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Chemically treated DNA repair gene fragment#35.
                                  ABL92260 standard; DNA; 6227 BP
                                                                                 01-JUL-2002
                                                         ABL92260;
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           RESULT 15
ABL92260/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reluxaemia, Alzheimer's disease, Alz, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 TITITITIATACAAAAAAAAATAATACAACACAATATTAATTGTGTTGTGTTATAAGGTGTTATAAT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, immune system disease, cytosine methylation, antiasthmatic; antiansemic; cytostatic; nootropic; neuroprotective, anti-HIV; anticonvulsant; obhthalmologic; anti-HIV; anticonvulsant; obhthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antistemency; cancer; eye disease; arterioscalerosis; anaemia; acute myeloid leukaemia; Alteimer's disease; ALDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.4%; Score 48.2; DB 6; Length 6227; Best Local Similarity 53.4%; Pred. No. 0.85; Matches 101; Conservative 0; Mismatches 88; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1559; 32pp + Sequence Listing; German
                                                                                          system associated gene SEQ ID NO: 1559.
                                                                                                                                                                                                                                                                                                                                                                                       Berlin K;
RESULT 14
ABL33586/c
ID ABL33586 standard; DNA; 6227 BP.
                                                                                                                                                                                                                                                                                                     02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 CAACACAAT 224
                                                                                                                                                                                                                                                                                                                                                             EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-130909/17
                                                                                                                                                                                                                                                     WO200200928-A2
                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              methylation.
                                                                      26-MAR-2002
                                                                                                                                                                                                                                                                              03-JAN-2002
                                              ABL33586;
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The invention relates to nucleic acids containing a sequence of at least 18 mucleotides of chemically treated DNA of genes associated with DNA repair, and their complements. The invention also relates to nucleic acids comprising at least 18 base pairs of the chemically pretreated DNA of genes associated with DNA repair selected from PMS2L1, PMS2L12, PMS2L12, PMS2L2, PMS2L2, PMS2L3, PMS2L3, PMS2L3, PMS2L3, PMS2L3, PMS2L3, PMS2L3, PMS2L3, PMS2L1, PMS2L3, PMS2L
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DNA repair; cytosine methylation; PMS2L1; PMS2L12; PMS2L2; PMS2L3; PMS2, L4; PMS2L5; PMS2L6; MGMT; MSH2; NUDT1; TDG; INPPL1; RFC4; DDIT1L; FANCB; RFCC8; ataxia telangiectasia; aging; Bloom's syndrome; Cockayne syndrome; Nijmegen breakage syndrome; Warner syndrome; immunodeficiency; trichthiodystrophy; Fanconi's anaemia; solid tumour; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid derived from genes associated with DNA repair, useful for diagnosis, e.g. of ataxia telangiectasia, by determination of cytosine methylation.
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07-APR-2000; 2000DB-010173.
30-JUN-2000; 2000DB-01043826.
01-SEP-2000; 2000DB-01043826.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                  Unidentified
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<sup>216</sup> CAACACAAT 224

<sup>2341</sup> AACATAAAT 2333

Search completed: February 28, 2004, 07:22:26 Job time : 363.627 secs

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Sequence 2, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 135, Appl
Sequence 135, Appl
Sequence 1559, Appl
Sequence 162, Appl
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Sequence 426, App
                                                                                                                                                                           February 28, 2004, 07:07:41; Search time 274.782 Seconds (without alignments) 3268.988 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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GenCore version 5.1.6
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US-10-424-599-137579
US-10-311-455-35
US-10-311-455-3
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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249
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Perfect score:
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Sequence 1832, Appli
Sequence 1832, Appli
Sequence 69, Appli
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Sequence 100, App
Sequence 136, App
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78 14 US-10-21-21-23-28-1-2
78 14 US-10-21-21-23-5
78 14 US-10-31-28-1492
14 US-10-240-845-176
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14 US-10-240-85-166
14 US-10-240-485-166
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14 US-10-311-455-659
16 US-10-311-455-149
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CACAATATTAATTGTGTTTTTAGGTGTTTATAATATATAAATCTAGGGGTTTAACGC
Sequence 4, Application US/08895435

Sequence 4, Application US/08895435

Publication No. US20030113837A1

Publication No. US20030113837A1

APPLICANT: Shamart, A. F. APPLICANT: And T. Engine Recombinase for Genetic Engineering FILE REPERENCE: 9882-012-99

CURRENT APPLICATION NUMBER: US/09/895,435

CURRENT FILING DATE: 2001-06-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.0

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGTACCGCCAGCATTTCGGAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAG
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100.0%; Score 249; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.6e-40;
Matches 249; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
, ORGANISM: Bacillus thuringiensis
US-09-895-435-4
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Best Local Similarity 100.
Matches 118; Conservative
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  181 AACACAATTTATCGATAAATAATACTTTTAGACGCAACACAATTTATAGACGCGGAGGA 240
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Publication No. US20030113837A1
General InfoRMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: Hallet, B.
TITLE CONT. Hallet, B. New Tyrosine Recombinase for Genetic Engineering
FILE REFERENCE: 9882-012-99
CURRENT APPLICANT: Now Tyrosine Recombinase for Genetic Engineering
FILE REFERENCE: 9882-012-99
CURRENT APPLICANTION NUMBER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 118
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                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, B. F.
APPLICANT: Stewart, B. T.
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REFERENCE: 9882-012-999
CURRENT PEPLICANT: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO1: 244
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2.6e-39;
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100.0%; Pred. No. :
tive 0; Mismatch
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Publication No. US20030113837A1
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; ORGANISM: Bacillus thuringiensis
US-09-895-435-2
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CRGANISM: Bacillus thuringiensis
US-09-895-435-1
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Best Local Similarity 100.
Matches 244; Conservative
                                             241 AATCACATG 249
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DB 10; Length 118;

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                                                                                                                                                                                                       61 TTTAACGCAACACATTTATCGATAAATAATACTTTTAGACGCAACACAATTTATAG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09895435
Publication No. US20030113837A1
GENERAL INFORMATION:
APPLICANT: Stewart A. F.
APPLICANT: Zhang, Y.
APPLICANT: Alallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 9882-012-999
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: STEWARTON:
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT FILEM DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
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100.0%; Pred. No. 1.8e-14; ive 0; Mismatches 0;
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Best Local Similarity 99.1%; Pred. No. 9.5e-14;
Matches 115; Conservative 0; Mismatches 1.
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Pred. No. 9.5e-14;
0; Mismatches 1
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CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
IENGTH: 116
TYPE: DNA
CORGANISM: Bacillus thuringiensis
US-09-895-435-8
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Best Local Similarity 99.1%;
Matches 115; Conservative
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                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_95242C.1 US-10-424-599-137579
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PRIOR APPLICATION NUMBER: PCT/EPO1/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
  113 TAATACAACACAATATTAATTGTGTTGTATTA
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LENGTH: 761
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; Sequence 10, Application US/09895435
; Sequence 10, Application US/09895435
; Publication No. US20030113837A1
; GENERAL INPORMATION:
; APPLICANT: Stewart, A. F.
; APPLICANT: Stewart, A. F.
; APPLICANT: Allet, B.
; TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
; FILE REPERBRED: 9882-012-999
; CURRENT APPLICATION NUMBER: US/09/895,435
; CURRENT FILING DATE: 2001-06-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 10
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Publication No. US20030113837A1

GENERAL INFORMATION:

APPLICANT: Schwart, A. F.

APPLICANT: Alallet, B.

APPLICANT: Hallet, B.

APPLICANT: Hallet, B.

APPLICANT: BALLet, B.

APPLICATION NUMBER: US/09/895,435

CURRENT FILING DATE: 2011-06-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.0

SEQ ID NOS: 10
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     173 TITTAACGCAACACAATITTATCGATAAATACTTTTTAGACGCAACACAATTTAT 228
                                             TITAACGCAACACAATITATCGATAAATAAATACTITTAGACGCAACACAATITAT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 TITAACGCAACACAATITATCGATAAATAATACTITITAGACGCAACACAATITAT 228
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Pred. No. 0.0009;
0; Mismatches 52; Indels
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Pred. No. 0.35;
0, Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEATURE:

NAME/KEY: N region

LOCATION: 33 ... 64

OTHER INPORMATION: n = a, t, g, or c

LOCATION: 81 ... 100

LOCATION: 81 ... 100

US-09-895-435-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Bacillus thuringiensis
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Best Local Similarity 65.6%;
Matches 82; Conservative
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NAME/KEY: N region
LOCATION: 37 . 74
OTHER INFORMATION: n = a, t,
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Best Local Similarity 55.2
Matches 64; Conservative
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Sequence 35, Application US/10311455
Sequence 35, Application US/10311455
Sublication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Otosine methylation
FILE OF INVENTION: cytosine methylation
FILE REPERBNCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 137579, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yould David K
APPLICANT: Cao Youngwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: 105/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                    61 NNNNNNNNNNNNNNACGCAACACATTTA-CGATAAATAATAATTGGCCGAACACA 119
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Gaps
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APPLICANT: OLEX, Alexander
APPLICANT: OLEX, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TILLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete:
TILLE OF INVENTION: Oytosine methylation
FILLE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILLING DATE: 2001-07-02
PRIOR FILLING DATE: 2001-07-02
PRIOR FILLING DATE: 2000-06-30
PRIOR PAPLICATION NUMBER: DE 10043826.1
PRIOR PLING DATE: 2000-09-01
PRIOR PLING DATE: 2000-09-01
SPIOR PLING DATE: 2000-09-01
SPIOR PLING DATE: 2000-09-01
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US-10-311-455-1559
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Best Local Similarity 53.4%; Pred. No. 4;
Matches 101; Conservative 0; Mismatches 88; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLEK, Alexander APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BIRLIN, Kurt TITLE OF INVENTION: Diagnosis of Diseases Associated with TITLE OF INVENTION: Metastasis CURRENCE: 5013.1007 CURRENCE: 5013.1007 CURRENT APPLICATION NUMBER: US/10/240,485
                                                        3636 acadadraracarcarananaarrrancacantricanca 3597
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PRIOR APPLICATION NUMBER: PCT/EP01/03970
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR PLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                     Sequence 1559, Application US/10311455 Publication No. US20030143606A1
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ORGANISM: Artificial Sequence
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APPLICANT: OLEK, Alexander
APPLICANT: DLEK, Alexander
APPLICANT: DLEK, Alexander
APPLICANT: DLEK, Alexander
APPLICANT: DEFENBROCK, Christian
APPLICANT: DLEK, Kurt
TITLE OF INVENTION: Cytosine methylation
FILE REPERENCE: 5013.104
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PLING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 3330
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                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
19.6%; Score 48.8; DB 14; Length 9642;
Best Local Similarity 51.4%; Pred. No. 3.5;
Matches 113; Conservative 0; Mismatches 107; Indels 0;
                                                                                                                                                                                                              Score 49; DB 14; Length 9905; Pred. No. 3.2; 0; Mismatches 110; Indel8
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Publication No. US20030143606A1
GENERAL INFORMATION:
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SEQ ID NO 35
LENGTH: 9905
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                              20017 March
Best Local Similarity 51.1%;
Matches 115; Conservative
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US-100-311-455-426/C
103-10-426, Application US/10311455
1 Sequence 426, Application US/10311455
1 Sequence 426, Application US/20030143606A1
2 Sequence 426, Application No. US20030143606A1
3 September No. US20030143606A1
3 APPLICANT: PIEPENBROCK, Christian
4 APPLICANT: PIEPENBROCK, Christian
5 APPLICANT: BERLIN, Kurt
7 TILE OF INVENTION: Cytosine methylation
7 TILE OF INVENTION: UNMBER: US/10/311,455
7 CURRENT FILING DATE: 2001-07-02
7 PRIOR FILING DATE: 2001-07-02
7 PRIOR PELICATION NUMBER: DE 10032529.7
7 PRIOR PELICATION NUMBER: DE 1004326.1
7 PRIOR PELICATION NUMBER: DE 1004326.1
7 PRIOR PELICATION NUMBER: DE 1004326.1
7 PRIOR APPLICATION NUMBER: DE 1004326.1
                                                    Sequence 3, Application US/10311455
Publication No. US20030143666A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DIEPETBROCK, Christian
APPLICANT: PIEPETBROCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
APPLICANT: OLINVENTION: Diagnosis of Diseases Associated with the Immune System by Dete
TITLE OF INVENTION: Cytosine methylation
FILE REPERBROCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DE 1003-25-2-6
PRIOR APPLICATION NUMBER: DE 1003-52-9.7
PRIOR FILING DATE: 2000-0-0-3
PRIOR FILING DATE: 2000-0-0-1
PRIOR FILING DATE: 2000-0-0-1
NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-0-0-0-1
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 3
LENGTH: 6072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-3
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18.8%; Score 46.8; DB 14; Length 6072;
Best Local Similarity 52.6%; Pred. No. 7.6;
Matches 102; Conservative 0; Mismatches 92; Indels 0;
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ORGANISM: Artificial Sequence
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Sequence 1, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Disagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: BO1/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
NUMBER OF SEQ ID NOS: 2
SEQ ID NOS: 2
SEQ ID NO 1.
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19.0%; Score 47.2; DB 14; Length 3673778;
Best Local Similarity 54.7%; Pred. No. 42;
Matches 94; Conservative 0; Mismatches 78; Indels 0; G
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                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-162
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47.2; DB 14; Length 18585;
Pred. No. 8.8;
0; Mismatches 88; Indels 0;
PRIOR APPLICATION NUMBER: DE 10032529.7 PRIOR FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: DE 10043826.1 PRIOR FILING DATE: 2000-09-01 NUMBER OF SEQ ID NOS: 202 LENGTH: 18585
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.2%;
Matches 100; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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; LOCATION: (3294164)
US-10-312-841-1
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; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-426
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	Gaps	ATTAT
.10869	0;	ATATAT
Length	Indels	ATCAGAAA
3 14;	87;	FAAAA
Query Match 18.8%; Score 46.8; DB 14; Length 6980;	best bodal Similarity 53.2%; Fred. NO. 7.5; Matches 99; Conservative 0; Mismatches 87; Indels 0; Gaps 0;	16 TITCGGAAAAAACCACGCTAAGAAATCAGAGTTAAAAAATCAGAAAATATATAT
18.8%;	53.2%; ative	AAACCACGC
1	Conserv	TCGGAAAA
tch	ar 5111 99;	16 TT
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<sup>76</sup> TCCTTGACACATACATGTTCTTTTTTATACAAAAATAATACAACACAATATTAATTGT 135

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<sup>6858</sup> ICICIAAAACAITIAITITAITIAAAAITACGACAIAAACAIAIAITIT 6799 6798 ATTTTTATAAATCTAAAAAAAAAAATTTTTAATAATTTTAATACAAATAAATAAAA 6739 136 GITGIAITAGGIGITATAAAATATAAAATCIAGGGGITTAACGCAACACAAITTAICGA 195

<sup>196</sup> TAAATA 201

<sup>6738</sup> AAAATA 6733

Search completed: February 28, 2004, 09:12:59 Job time: 285.282 secs

Run on:

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; Search time 3916.83 Seconds (without alignments) 2236.845 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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pna/US6019 COMB. seq:
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Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence Seq	
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Score	11111 1111	OUNT 100-895-435-4 109-895-435-4 SEQUENCE 4, R SENERAL INFOS APPLICANT: APPLICANT:
Result No.	NBS	Sequence ; Sequence ; GENERAL I APPLICAN ; APPLICAN ; APPLICAN

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RESULT 1
US-09-895-435-4
Sequence 4, Application US/09895435
Sequence 4, Application US/09895435
GENERAL INFORMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Allet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REFERENCE: 988-012-999
CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 249
TYPE: DNA
CORGANISM: Bacillus thuringiensis
US-09-895-435-4
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                                                          GGGGTACCGCCAGCATTTCGGAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAG
                                                                               121 CACAATATTAATTGTGTTTGTATTAGGTGTTATAATAATATAAATCTAGGGGTTTAAACGC
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APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REPERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435A
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
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100.0%; Score 249; DB 36;
Best Local Similarity 100.0%; Pred. No. 8.3e-36;
Matchés 249; Conservative 0; Mismatches 0;
100.0%; Score 249; DB 36;
100.0%; Pred. No. 8.3e-36;
ive 0; Mismatches 0;
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US-09-895-435-1
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; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Bacillus thuringiensis
 Query Match 100.
Best Local Similarity 100.
Matches 249; Conservative
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  121 CAATATTAATTGTGTTGTATTAGGTGTTATAATAATATAAAATGTAGGGGTTTAACGCAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 ITTAACGCAACACAATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAG 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Stewart, A. F.
APPLICANT: Stewart, Y. F.
APPLICANT: Stewart, Y. APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435A
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Stewart, A. F.
APPLICANT: Stewart, Y.
APPLICANT: Hallet, Y.
APPLICANT: Hallet, Y.
APPLICANT: Hallet, Y.
APPLICANT: Hallet, Y.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 9882-012-999
FILE REFERENCE: 9882-012-999
FURRENT APPLICATION NUMBER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 118
TYPE: DNA
COGGANISM: Bacillus thuringiensis
US-09-895-435-2
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47.4%; Score 118; DB 36;
Best Local Similarity 100.0%; Pred. No. 5.6e-12;
Matches 118; Conservative 0; Mismatches 0;
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47.4%; Score 118; DB 36;
Best Local Similarity 100.0%; Pred. No. 5.6e-12;
Matches 118; Conservative 0; Mismatches 0;
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US-09-895-435A-2
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US-09-895-435-2
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Sequence 1, Application US/09895435A

SEQUENCE 1, Application US/09895435A

APPLICANT: Stewart, A. F.

APPLICANT: Annay, Y.

APPLICANT: Hallet, B.

TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering TITLE OF INVENTION: 982-012-999

CURRENT APPLICATION NUMBER: US/09/895,435A

CURRENT FILING DATE: 2001-06-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Version 3.0

SEQ ID NO 1

LENGTH: 244
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: Zhang, Y.
APPLICANT: Hallet, B.
APPLICANT: Hallet, B.
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 982-012-999
CURRANT APPLICATION WNBER: US/09/895,435
CURRANT FILING DAIR: 201-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
ENGTH: 244
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98.0%; Score 244; DB 36;
Best Local Similarity 100.0%; Pred. No. 6.7e-35;
Matches 244; Conservative 0; Mismatches 0;
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Pred. No. 6.7e-35;
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100.0%; Pred. No. c.
... 0; Mismatches
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CRGANISM: Bacillus thuringiensis
US-09-895-435-1
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CRGANISM: Bacillus thuringiensis
US-09-895-435A-1
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Best Local Similarity 100.
Matches 244; Conservative
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Sequence 7, Application US/09895435
GENERAL INFORMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 9882-012-99
CURRENT APPLICATION WHOBER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Version 3.0
SEQ ID NO 7
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APPLICANT: Stewart, A. F.
APPLICANT: Alallet, Y.
APPLICANT: Hallet, Y.
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REFERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOPTWARE: Patentin version 3.0
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45.9%; Score 114.4; DB 36
Best Local Similarity 99.1%; Pred. No. 2.5e-11;
Matches 115; Conservative 0; Mismatches 1.
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; ORGANISM: Bacillus thuringiensis
US-09-895-435-8
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Matches 115, Conservative
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Sequence 7, Application US/09895435A GENERAL INFORMATION:

US-09-895-435A-7

APPLICANT: Stewart, A. F. APPLICANT: Zhang, Y. APPLICANT: Hallet, B.

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113 TAATACAACACAATATTAATTGTGTTGTATTAGGTGTTATAATAATATAAATCTAGGGG 172
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GENERAL INFORMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Application Stewart, A. F.
APPLICANT: Alang, Y.
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: Hallet, B.
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REFERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435A
CURRENT APPLICATION NUMBER: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFREENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435A
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
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Pred. No. 2.5e-11;
0; Mismatches 1; Indels
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Pred. No. 2.5e-11;
0; Mismatches 1
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; ORGANISM: Bacillus thuringiensis
US-09-895-435A-8
                                                                                                                                                                                                      TYPE: DNA; CRGANISM: Bacillus thuringiensis
US-09-895-435A-7
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SEQ ID NO 9
LENGTH: 116
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Best Local Similarity 99.1%;
Matchés 115; Conservative (
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Best Local Similarity 99.1%;
Matches 115; Conservative
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US-09-895-435A-8
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LENGTH: 116
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Hridayabhiranjan
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: De Pena, Robert C.
APPLICANT: Bougri, Olegs
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9. Application US/09895435A
GENERAL INFORMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REFERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435A
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
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Pred. No. 0.038;
0; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Indels
                                                                                                                                                                                                                                                                                                                                                                                 DB 36;
                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 3
Pred. No. 0.038
0; Mismatches
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OTHER INFORMATION: n = a, t, g, or FEATURE:
NAME: N region
LOCATION: N 1 ... 100
OTHER INFORMATION: n = a, t, g, or
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ORGANISM: Bacillus thuringiensis
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                                                                NAME/KEY: N_region

LOCATION: 33 ... 64

OTHER INFORMATION: n = a, t, g, independent in the control in the cont
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Best Local Similarity 55.2%;
Matches 64; Conservative
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al Similarity 55.2%;
64; Conservative
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Best Local Similarity
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NAME/KEY: N region
LOCATION: 33 . . 64
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Sukra, Joseph R.
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Bougri, Olegs
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51892)B
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/197,872
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 81288
SEQ ID NO 69057
LENGTH: 382
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Pred. No. 7.6;
0; Mismatches 96;
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US-09-837-604B-69057
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NAMB/KEY: unsure
LOCATION: (1)..(382)
OCHER INFORMATION: unsure at all n locations
FEATURE:
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OTHER INFORMATION: unsure at all n locations
FILE REFERENCE: 38-21(51892)B
CURRENT APPLICATION VMBER: US/09/837,604A
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/197,872
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 81288
SQ ID NO 69057
LENGTH: 382
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ORGANISM: Oryza sativa nipponbare
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ORGANISM: Oryza sativa nippombare
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Best Local Similarity 51.5%;
Matches 102; Conservative
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us-09-895-435a-4.rnpm

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Byrum, Joseph R.
De La Pena, Robert C.
La Rosa, Thomas J.
Shukla, Hridayabhiranjan
Nucleic acid Molecules and Other molecules associated with
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                                                                                                  TGTTGTATTAGGTGTTATAATAATATAAATCTAGGGGTTTAACGCAACACAATTTATCG 194
                                                                                                                                                                             15 ATTICGGAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAATCAGAAAATATATCATTA
15 ATTTCGGAAAAAAACCACGCTAAGAAAATCAGAGTTAAAAAAATCAGAAAATATATCATTA
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20.7%; Score 51.6; DB 75; Length 382;
Best Local Similarity 51.5%; Pred. No. 7.6;
Matches 102; Conservative 0; Mismatches 96; Indels 0
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                                                                                                                                                                                                                   195 ATAAATAATACTTTAG 212
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US-60-197-872-65927
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Search completed: February 28, 2004, 10:49:21 Job time : 3918.83 secs

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Sequence 5, Application US/10765790 GENERAL INFORMATION:
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APPLICANT: Beard, Chris
APPLICANT: Beard, Chris
APPLICANT: Gannon, Allison
APPLICANT: Harvey, Jeanne
APPLICANT: Lechner, John F.
APPLICANT: Lichner, John F.
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US-10-765-790-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Juence 1, Appli
Sequence 43, Apri
Sequence
                                                                                                                                                                                          February 28, 2004, 07:22:37; Search time 42.7439 Seconds (without alignments) 981.354 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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6 US-10-765-790-5
6 US-10-417-375A-146
6 US-10-767-471-10700
6 US-10-767-471-10680
6 US-10-767-471-10810
6 US-10-767-471-10810
6 US-10-767-471-10810
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6 US-10-767-471-10806
6 US-10-767-471-10806
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US-10-765-790-48
US-10-76-7471-10561
US-10-76-7471-10675
US-10-76-7471-10675
US-10-76-7471-10652
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US-10-76-7471-10652
US-10-76-7471-10652
US-10-76-7471-10652
US-10-76-7471-10915
US-10-76-7471-10915
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US-10-767-701-17775
US-10-767-471-10713
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US-10-767-471-10601
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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16.8 380963 6

16.1 803757 6

15.9 43868 6

15.7 15286 6

15.7 19445 6

15.3 1790242 6

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15.1 36104 6

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14.7 189317 6

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14.6 15344 6

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14.5 47459 6

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Match Length DB
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Perfect score:
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Maximum DB seq
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US-10-767-471-41924 Sequence 519, Approx 2001, 2010-501, Approx 2010-501, Sequence 510, Approx 2010-65-790-103 Sequence 510, Approx 2010-765-790-103 Sequence 103, Approx 2010-765-790-73 Sequence 10668, Approx 2010-765-790-73 Sequence 387, Approx 2010-765-790-5 Sequence 5, Approx 2010-765-790-5 Sequence 10619, Approx 2010-767-471-10619 Sequence 10619, Approx 2010-767-471-10619 Sequence 10619, Approx 2010-767-471-10619 Sequence 10619, Approx 2010-767-471-10619 Sequence 261, Approx 2010-765-790-106 Sequence 261, Approx 2010-765-790-106 Sequence 261, Approx 2010-765-791-10650 Sequence 261, Approx 2010-767-471-444 Sequence 444, Approx 2010-767-471-444 Sequence 443, Approx 2010-767-471-444 Sequence 443, Approx 2010-767-471-444 Sequence 243, Approx 2010-767-471-471	NMENTS  cules and Other Molecules Associated Wit Thereof For Plant Improvement  7.701	imilarity 54.0%; Pred. No. 1; Conservative 0; Mismatches 75; Indels, 0; Gaps 0; Conservative 0; Mismatches 75; Indels, 0; Gaps 0; Mismatches 75; Indels, 0; Gaps 0; Mismatches 75; Indels, 0; Gaps 124
US-110-76	ALIG /1076770 cid Mole nd Uses S/10/767 -29	; Score 4 ; Pred. N O; Mism Acacaracar Adaradaba Adaracaracar Adaracaracar Adaracaracaracaracaracaracaracaracaracara
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44444444444444666666666666666666666666	701-20322 20322, Application INT Royalic). NT: Kovalic). NT: Zhou, Yihua NT: Cao, Yongwei F INVENTION: NUBER F INVENTION: NUBER F FILING DATE: 200 OF SEQ ID NOS: 631. 0 641 DNA SM: SOZGHUM bicolo SM: SOZGHUM bicolo E: INFORMATION: Clone INFORMATION: Clone INFORMATION: Clone	Similarity Similarity TATATCATU TGTATCATG TGTATCATG ATATTAATT AGATTTTAAC CAATTTAAC AATTCATG
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TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
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                                                                                                                                                                                                                                              DB 6; Length 380963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-417-375A-146
) Sequence 146, Application US/10417375A
SEMERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
ITILE OF INVENTION: Novel Therapeutic Targets in Cancer;
FILE REFERENCE: 529452001600
CURRENT PILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 146
LENGTH: 350570
                                                                                                                                                                                                                                                                              52; Indels
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Pred. No. 1.8;
0; Mismatches
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             FILE REPERENCE: 1657/2035
CURRENT APPLICATION NUMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
PRIOR PPLICATION NUMBER: US 10/737,082
PRIOR FLING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
SOFURARE: PatentIn version 3.2
LENGTH: 380963
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NAME/KEY: misc_feature

LOCATION: (1)...(350570)

CTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 58.4%;
Matches 73; Conservative
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Matches 95; Conservative
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CRGANISM: Homo sapiens
US-10-765-790-5
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// NAME/KEY: misc_feature
// DOCATION: (1)...(803755)
// OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables :
US-10-767-471-10700
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| DOCATION: (1)...(43868)

| OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables

US-10-767-471-10680
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Sequence INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERAL COLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATIOD ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001565
CURRENT PELLING NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FRAESEQ for Windows Version 4.0
SOFTWARE: FRAESEQ for Windows Version 4.0
LENGTH: 43868
                                        APPLICANT: CARGILL, Michele et al TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01505 CURRENT APPLICATION NUMBER: US/10/767,471
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Best Local Similarity 51.7%; Pred. No. 4.6;
Matches 90; Conservative 0; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 803755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
16.1%; Score 40; DB 6; Length 803
Best Local Similarity 50.0%; Pred. No. 4;
Matches 100; Conservative 0; Mismatches 100; Indels
                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 5024-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10700
LENGTH: 803755
TAYDE. T...
Sequence 10700, Application US/10767471 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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NAME/KEY: misc_feature

) LOCATION: (1)...(166020)

) OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables

US-10-767-471-10806
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Sequence 10806, Application US/10767471

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENERALIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: GENERALIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERRACE: CL001505

CURRENT FILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 50231

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10806

LENGTH: 166020
                                                                                                                                                                                                                                                                                                                                               Sequence 10714, Application US/10767471
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION:
GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FASTSEQ for Windows Version 4.0
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6980 ATATATTTTATAAAACAAATAATATTTTTTTATAATTATATAAACAAATAA 7039
                                                    134 GIGITGIATTAGGIGITATAATATATAAATCTAGGGGTTTAACGCAACACAATTTATC 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39.2; DB 6; Length 99445; Pred. No. 5.6; 0; Mismatches 58; Indels 0;
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Best Local Similarity 56.1%;
Matches 74; Conservative (
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CORGANISM: Homo sapiens
US-10-767-471-10714
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US-10-767-471-10806/c
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US-10-767-471-10714
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LENGTH: 99445
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NAME/KEY: misc_feature

1.05ATION: (1)...(109977)

COCATION: (1)...(109977)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-767-471-10722
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Sequence 10810, Application US/10767471

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: REDWATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1505

CURRENT APPLICATION NUMBER: US/10/767,471

CURRENT FILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 50231

SOFTWARE: PSELSEQ for Windows Version 4.0

SEQ ID NO 10810
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001505

CURRENT APPLICATION NUMBER: US/10/767,471

CURRENT FILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 50231

SOFTWARES FRASEQ for Windows Version 4.0

SEQ ID NO 10722

LENGTH: 109977
                                                                                <u> 33890 ААААТАТСТАААТАТАССААТАТТАТАТАСААССТТААААСТТААААТСТТТАТАТАААА</u> 33949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 AAAATCAGAAAATATATCATTATTCCTTGACACATACATGTTCTTTTTTTATACAAAAA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                       124 AATATTAATTGTGTTTATAGGTGTTATAAATATAAATCTAGGGGTTTAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%; Score 39.4; DB 6; Length 109977; 56.6%; Pred. No. 5.1; tive 0; Mismatches 56; Indels 0;
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15.7%; Score 39.2; DB 6; Length 5:
Best Local Similarity 56.1%; Pred. No. 5.5;
Matches 74; Conservative 0; Mismatches 58; Indels
                               64 ATATATCATTATTCCTTGACACATACATGTTC
                                                                                                                                                                                                                                                                                                                          Sequence 10722, Application US/10767471
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.8
Best Local Similarity 56.6
Matches 73; Conservative
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ORGANISM: Homo sapiens
US-10-767-471-10810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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ठे d D ð Gaps

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i LOCATION: (11...(1790242)
i OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables :
US-10-767-471-10805
. LOCATION: (1)...(41514)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1 US-10-767-471-10654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHODS OF DETECTION AND USES THEREOF
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GENERAL INFORMATION:
ARPLICANT: Kovalio, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Chou, Yihua
TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 ACACATACATGITCITITITATACAAAAATAATACAACACAATATTAATTGIGITGIA 141
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Pred. No. 9.3;
0; Mismatches 105; Indels 0;
                                                                                                          Length 41514;
                                                                                                                                                    75; Indels
                                                                                                                                                                                                    52 AAAAATCAGAAATATATCATTATTCCTTGACACATACATGTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETE
FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SEQ ID NOS: 50231
SEQ ID NO 10805
LENGTH: 1790242
                                                                                                                                                                                                                                                                                                                                                                                                                               20801 TAPATATATATATATGTTTATATAAATATATATAT 20838
                                                                                                        Score 38; DB 6;
Pred. No. 9.3;
0; Mismatches 7.
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Sequence 10805, Application US/10767471
GENERAL INFORMATION:
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Best Local Similarity 49.0%;
Matches 101; Conservative
                                                                                                          Query Match
Best Local Similarity 52.5%;
Matches 83; Conservative
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US-10-767-701-17775/c
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// OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-767-471-10805
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GENERAL INFORMATION:
APPLICANT: CREGILL, Michele et al APPLICANT: CREGILL, Michele et al TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: RHEDWATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF FILE REPRENCE: CLOO1505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOUTHARE: FastSEQ for Windows Version 4.0
LENGTH: 41514
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10805, Application US/10767471
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michale et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01505
CURRENT APPLICATION UNMER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FREUESE for Windows Version 4.0
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                                                                                                                                                                                   97 ITITITIATACAAAAATAAAACACAATATTAATTGTGTTGTATTAGGTGTTATAATA
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Pred. No. 8.5;
0; Mismatches 73; Indels 0;
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                                                                                                                                                                                                                                                                                                                      17296 TATATATATATAA 17282
                                                                                                                                                                                                                                                                             217 AACACAATTTATAGA 231
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Best Local Similarity 52.9%;
Matches 82; Conservative
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
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TENGTH: 1790242
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TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (1).__(36106)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-767-471-10713
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1505
CURRENY APPLICATION NUMBER: US/10/767,471
CURRENY FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SEQ ID NO 10713
LENGTH: 36106
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                                                                                                                                                                                                                                                                                                                                                                        128 ABABARCTARARARATARARARATARARARARARATATARARARTATARARARARARARA 369
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Pred. No. 11;
0; Mismatches 69; Indels 1;
                                                                                                                                                                                                                                                 Score 37.8; DB 6; Length 447; Pred. No. 9.5; 0; Mismatches 107; Indels
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; OTHER INFORMATION: Clone ID: LIB3476-047-P1-K1-D11
US-10-767-701-17775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 ATAAGAAAATAGAACACTATATAGACA 220
FILE REFERENCE: 38-21(53535)B
CURRENT PAPLICATION NUMBER: US/10/767,701
CURRENT APLING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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Best Local Similarity 56.2%;
Matches 90; Conservative
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Best Local Similarity 48.8%;
Matches 102; Conservative
                                                                                                                  TYPE: DNA
ORGANISM: Sorghum bicolor
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ORGANISM: Homo sapiens
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                     CURRENT APPLICA:
CURRENT FILLING I
NUMBER OF SEQ II
SEQ ID NO 17775
LENGTH: 447
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RESULT 15

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APPLICANT: Burges, Chris
APPLICANT: Burges, Chris
APPLICANT: Gannon, Allison
APPLICANT: Gannon, Allison
APPLICANT: Hechner, John F.
APPLICANT: Lechner, John F.
APPLICANT: Li, Zheng
TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
FILE REFERENCE: 1657/2035
CURRENT APPLICATION NUMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
SOFTWARE: Patentin version 3.2
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Pred. No. 11;
0; Mismatches
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ne : 51.7439 secs
, Application US/10765790
                         ENERAL INFORMATION:
APPLICANT: Bayer Healthcare LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.1%;
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Best Local Similarity 53.4
Matches 79; Conservative
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US-10-765-790-48
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LENGTH: 156652
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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BX417261/c
LOCUS
DEFINITION
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AL097152 Drosophil
AL066199 Drosophil
BX338369 BX338369
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249
1 ggggtaccgccagcatttcg......gacgcggaggaaatcacatg 249
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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                                                                                                                           OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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AL104456 Drosophil AL208909 Tetraodon BX339264 BX339264 BX359378 BX359378 AL03539 Drosophil	BX334085 BX334085 AL099163 Drosophil BX462207 BX462207	AL100526 Drosophil BX456623 BX458623 AU074022 AU074022	AX36885 BX436885 BX359398 BX359398 AL063632 Drosophil AL105023 Drosophil	AL074369 Drosophil AL099422 Drosophil AL106008 Drosophil AL429343 clone BA0 BX439779 BX439779	AL229845 Tetracdon AL064091 Drosophil AQ092950 HS_3005_A BM891761 sam43£11. AQ393140 CITBI-E1- AL05232 Drosophil BX401903 BX401903 BX458623 BX458623	EX403499 EX403499 CE144436 tigr-ges- BX380865 EX380865 BX353130 EX353130 BX425839 EX425839 AL108152 Drosophil AL064351 Drosophil	AL175696 Tetraodon CA972153 ACENCOURT BX417261 BX417261 BB420654 HWM001.B0 BX447434 BX447434
CNS014PQ CNS02Q6S BX339264 BX359378 CNS009G1	BX334085 CNS010MP BX462207	CNS0110K BX458623 AU074022	CNS01036 BX436885 BX359398 CNS000B8 CNS0155H	CNS 0 0 1 3 3 CNS 0 1 1 3 4 CNS 0 1 5 WU CNS 0 7 4 W 9 EX 4 3 9 7 7 9	CNS036CC CNS003BD AQ0950 BM891761 AQ393140 CNS0080F BX461903 BX461903	BX403499 CE144836 BX380865 BX3253130 BX425839 CNS017KE	CNS020K7 CA972153 BX417261 BE420654 BX447434
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## ALIGNMENTS

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	BX417261 1179 bp mRNA linear EST 13-MAY-2003
Z	BX417261 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE006YP16
	5-PRIME, mRNA sequence.
z	BX417261
	BX417261.1 GI:30650375
	. LDA
	Homo sapiens (human)
SM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
ш	1 (bases 1 to 1179)
တ	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
	Full-length cDNA libraries and normalization
ı	Unpublished (2001)
	Contact: Genoscope
	Genoscope - Centre National de Sequencage
	BP 191 91006 EVRY cedex - France
	Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
	Library was constructed by Life Technologies, a division of
	Invitrogen. This sequence belongs to sequence cluster 6333.r For
	more information about this cluster, see
	http://www.genoscope.cns.fr/
	cgi-bin/cluster.cgi?seq=CSODE006DH08QP1&cluster=6333.r. Contact :
	Feng Liang Email : fliang@lifetech.com URL :
	http://fulllength.invitrogen.com/ InVitroGen Corporation 1600

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Direct Submission

Submitted (102-UNN-1999) Genoscope - Centre National de Sequencage :

Submitted (102-UNN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo (soegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecogenic strain of Drosophila DNA provided by the BDGP from the isogenic strain v2; on w sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                             GSS 03-JUN-1999
                                                                                                                                                                                                                                                                        86 AIACAIGITCTTTTTTTACAAAAATAATACAACAATATTAATTGTGTGTTATTAG 145
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                                                                                                                                                                                                                                                                                                                                                                               926 bp DNA linear GSS 03-JUN-15
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14P07 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                                                                                                                     26 AAACCACGCTAAGAAAATCAGAGTTAAAAATCAGAAAATATATCATTATTCCTTGACAC
                                                                                                                                                                                                         Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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/db_xref="taxon:7227"
                                                                     ch 23.1%; Score 57.4; DB 29; I Similarity 39.7%; Pred. No. 0.57; 81; Conservative 39; Mismatches 84;
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Drosophila melanogaster
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/clone lib="RPCI-98"
/note="end : T7"
/note="end : SP6"
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Best Local 8
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                                                                                                                                                                             /tissue type="PLACENTA"
/clone lib="Home sapiens PLACENTA"
/clone lib="Home sapiens PLACENTA"
/ncle="Vector: pCMVSEORT 6, 1st strand cDNA was primed
with a NoII-oligo(dT) primer. Five prime end enriched,
with a NoII-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the NoI and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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- Web : www.genoscope.cns.fr)
Determination of this BAC-mas sequence was carried out as part of a collaboration with the European Droscphila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Droscphila melanogaster BAC ibrary (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Faraday Avenue Genoscope sequence ID : CSODEO06DH08QP1.
Location/Qualifiers
1. 1179
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                     organism="Homo sapiens"
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pg7 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN12P22 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (132-7011-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-en sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding proyided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 ACACATACATGTTCTTTTTTTATACAAAATAATACAACACAATATTAATTGTGTTGTA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 AATACTTTTAGACGCAACACAATTTATAGA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     910 WWWWAWTAAAAAAAAAAAAA 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="DrosBAC"
/clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
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GSS; genome survey sequence.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                          AL104456.1 GI:5616067
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995 TWATTTTTW 1004
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Best Local S:
Matches 75
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BX338369
BX338369.1 GI:30343682
BST.
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 ENRY Gedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of
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Library was constructed by Life Technologies Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODIO58DC07QP1.

Location/Qualifiers

Location/Qualifiers

//organism="Homo_sapiens"
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/db xref="taxon:9606"
/clone="CSODIO58F14"
/clone lib="PLACENTA COT 25-NORWALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/nore="lst strand cDNA was primed with a NorI-oligo(dT)
/nore="lst strand cDNA was primed with a NorI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Nor I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                    548
                                                                                                     82 ACACATACATGTTCTTTTTTTATACAAAAATAATACAACAACAATATTAATTGTGTTGTA 141
                                                                                                                                    549 WRATATATATTATTATTATTATANATRWGTWATDANWGATWAKTTATWTATTAWTWWT 608
                                                                                                                                                                                                         TRAGGIGITATAATAAATATAAATCTAGGGGTTTAACGCAACACAATTTATCGATAAATA 201
                                                                                                                                                                                                                                                             609 ICWGTATTTATATATATATTTTGATGWTATGWAAWTAAAWAWTAATATTGAGAAAAWR 668
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AAAAAAACCACGCTAAGAAAATCAGAGTTAAAAATCAGAAAATATATTCATTG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 TTAGGTGTTATAATAAATATAAAATCTAGGGGTTTAACGCAACACAATTTATCGATAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 AAAANACAAANCCAMAWAWAAWAAATTTTGWTAWATWWWTAAATATATATATTTTAAA
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                              202 AATACTTTAGACGCAACACAATTTATA 229
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
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Contact: Genoscope
Genoscope - Centre National de Sequencage
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/clone="CS0DI070YG16"
                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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Homo sapiens
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98; Conserva
                  sapiens
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BX339264 GI:30337783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cne.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, estinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Adanthomorpha, Adanthopterygii, Percomorpha, Tetraodontiformes, Tetradontoidea, Tetraodontidae, Tetraodon.
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                                                                                                Rocet Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetracdon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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                                                                                                                                                                                                                                                  Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Sauxin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of Freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
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/clone lib="G"
/note="Genoscope sequence ID : COAG157BA02SP1-end
PUC-OX:"
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    924
/organism="Tetraodon nigroviridis"
/nol_type="genomic DNA"
/db_xref="taxon:99883"

   Tetraodon nigroviridis
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDMs libraries and normalization
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li (bases 1 to 989)
Li W.B.; Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                Contact: Teacher National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8045.f For
http://www.genoscope.nn.fr/
cgi-bin/cluster.cgi?seq=CSODIO70BD08QPl&cluster=8045.f. Contact :
Feng Libral Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO70BD08QPl.
Location/Qualifiers
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45.0%; Pred. No. 2.7;
live 23; Mismatches 97;
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clone CSODI056YP18 5-PRIME, mRNA sequence.
BX359378
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45.9%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95; Conservative
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Matches 95
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Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage :
Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage :
BP 1919 19006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Petermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
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BP 191 91006 EVRY cedex - France main: sequencecope.cns.fr Enail: sequef@genoscope.cns.fr, web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL: http://fulllengfh.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODIO56DH09QP1.
                                                                                                                                                                                                                                                                                                                                   /moi_type="mRNA"
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/clone_Tib="Homo sapiens PLACENT
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster
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BX334085 1001 bp mRNA linear EST 02-MAY-2003
BX344085 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CSODD006YL06 5-PRIME, mRNA sequence.
BX334085
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primer. Five prime end enriched, double-strand cDNA_was
digested with Not I and cloned into the Not I and EcoR V
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(Dases I to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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BP 191 91006 EVRY cedax - France
BR 191 91006 EVRY cedax - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6562.r For
http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?aeq=CSODD006DF03QP1&cluster=6562.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD006DF03QP1.
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and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
__location/Qualifiers
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/mol Lyge="make" | Jan. | Jan.
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221
                                                                                                                                                                                                                                                                  BX462207 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA clone CS0DG004YB03 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
1 (bases 1 to 1201)
1 (h. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Contract: Genoscope.
Contract: Genoscope.
Contract Structure National de Sequencage
BP 191 91006 EVRY cedex - France
Interpretation appoint of the Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 24.r For moinformation about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODGO04CAO2QPI&cluster=24.r. Contact :
Feng Lind Email : fliangelifector.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODGO04CAO2QPI.
162 AATTITITIAAAWWMMTYAWAITITITIWIWAIWAAWMWTWAAAAWAAWAAWATIATAT
                                                         171 GGTTTAACGCAACACATTTATCGATAAATAAATACTTTTAGACGCAACA 220
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BX462207/c
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBPH (Centre for European Drosophila welanogaster BAC wordset with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                  76 TCCTTGACACATACATGTTCTTTTTTTATACAAAAATAATACAACACAATATTAATTGT 135
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AL099163. GI:5610774
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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sequence T7 end of BAC
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                                                                                      21.3%; Score 53; DB 13; Length 1201;
llarity 47.2%; Pred. No. 3.1;
Conservative 18; Mismatches 85; Indels
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/db_xref="taxon:7227"
/clone="BACN04L20"
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/plasmid="pBeloBAC11"
/note="end : T7"
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Contact: Genescope
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BP 191 91006 EVRY cedex - France
Interpose of This sequence belongs to sequence cluster 9800.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBE006AD02QPl&cluster=9800.f. Contact :
Feng Liang Email : fllang@lifetech.com VRL:
Feng Liang Email : fllang@lifetech.com / InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBE006AD02QPl.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol:tsukuba.ac.jp
PROJECT = Diccycstellum discoideum cDNA project in Japan.
Location/Qualifiers
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Unpublished (1999)
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Dictyostelium discoideum
Enkaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
1 (bases 1 to 240)
Urushihara,H.
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Institute of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="CS0DE006YG03"
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EX458623 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE006YG03
EX458623
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                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (8-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Bros BAC) was made by Alain Billaud at CEPH (Centre Indoorded of Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNS0110K
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN06G12 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 813)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.1%; Score 52.6; DB 29; Length Best Local Similarity 47.1%; Pred. No. 4.5; Matches 106; Conservative 15; Mismatches 104; Indels
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                                                                                                                                                                           Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                     fly), genomic survey sequence. AL100526
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                                                                                                                        AL100526.1 GI:5612137
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142 TTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGCAACACAATTTATCGATAAATA 201
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/dev stage="slug"
/dev stage="slug"
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Search completed: February 28, 2004, 09:05:55 Job time : 2941.47 secs

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February 28, 2004, 05:48:29; Search time 171.373 Seconds (without alignments) 2925.120 Million cell updates/sec
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Abz75336 B. thurin	Abz75335 B. thurin	Abz75338 B. thurin	ш	Abz75340 B. thurin	Abz75342 B. thurin	Abz75343 B. thurin	Ada73029 Rice gene	Abl34026 Human imm	Acf70232 Photorhab	Continuation (4 of	Continuation (5 of	Continuation (33 o	Continuation (34 c	Abl34027 Human imm	Aas46531 Tumour su	Abl32729 Human imm	Aak76448 Human imm	Aak76449 Human imm	Aaa32056 Plant mic	Abl32340 Human imm	Aad48244 Ehrlichia	Abl03956 Drosophil
ΩI	ABZ75336	ABZ75335	ABZ75338	ABZ75341	ABZ75340	AB275342	ABZ75343	ADA73029	ABL34026	ACF70232	ACF65385 3	ACF65385_4	ACF67367_32	ACF67367_33	ABL34027	AAS46531	ABL32729	AAK76448	AAK76449	AAA32056	ABL32340	AAD48244	ABL03956
DB	7	7	7	7	7	,	7	7	9	7	7	7	7	7	w	4	9	4	4	m	9	9	4
Length	118	244	249	116	116	116	124	2000	17594	750	110000	110000	110000	110000	17594	7008	14307	4421	4421	230	5349	2778	6651
% Query Match	100.0	100.0	100.0	6.96	6.96	54.2	43.2	35.4	33.2	32.2	32.2	32.2	32.2	32.2	31.9	31.7	31.4	30.8	30.8	30.0	29.8	29.5	29.2
Score	118	118	118	114.4	114.4	64	51	41.8	39.5	38	38	38	38	38	37.6	37.4	37	36.4	36.4	35.4	35.2	34.4	34.4
Result No.	Т	7	m	4	Ŋ	9	7	ω υ	σ	10	c 11	c 12	c 13	Ω 14	c 15	c 16	c 17	c 18	c 19	20	c 21	22	c 23

Abl03922 Drosophil Abl32655 Human imm Abl32655 Human imm Abl32655 Human imm Abl32668 CDNA enco Abl34613 Human met Abl34613 Human imm Abl70603 Chemicall Abz75338 B. thurin Abzz7534 B. thurin Abzz7534 B. thurin Abzz7534 Human imm Abzz255 Chemicall Abz7531 Human imm Abz7531 Human imm Abz7531 Cat flea Aac93751 Cat flea Aac93751 Cat flea				sequence TRI'.	<pre>['; genetic engineering;</pre>			-									I and the recombination substrate c engineering, Inpl-mediated py.
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ABL03922 ABL333732 ABL33632 AAK91250 ABC492641 ABC492641 ABL34613 ABL34613 ABL75335 ABL75335 ABL71154 ABL21158 ABL21158 ABL21158 ABL31131 ABL31433 ABL3643 ABL	ALIGNMENT	BP.		ry) ecognition ta	nase; TRT ''; ds.		alifiers INVERTED		DIRECT			. 9		IOLOGY LAB. LOUVAIN.	et B;		combinas ul for g or gene
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000_00000		RESULT ABZ7533 ID AE	Z X E	EXE	<b>₹</b> ₹₹	<b>383</b>	1111 <b>1</b>	FFFFF	####	2 E S	8	44 Y	1 H ;	888	<b>1</b>	<b>183</b>	\$255X

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               The invention relates to a novel composition comprising an isolated DNA molecule comprising Tmp1 recombination substrates. The composition may have a use in gene therapy, and as a vaccine. The recombination substrates TRI or TRI' sequences are useful for genetic recombination. The title are useful for Tmp1—mediated genetic recombination. The Tmp1—mediated site-specific recombination is useful for deleting or inserting DNA sequences to modulate gene expression, integrating new incleotide sequences into a DNA molecule, such as an episome or genomic DNA, for gene therapy, or for producing food-grade genetically modified organisms. The present sequence represents the Tmp1 recognised target
                                                                                                                                                                                          61 TITAACGCAACACAATITATCGATAAATAATACTITITAGACGCAACACAATITATAG 118
                                                                                                                                                                                                                                                  61 TTTAACGCAACACAATTTATCGATAAATAAATACTTTTAGACGCAACACACATTTATAG 118
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TnpI recognised target, TRT'', ds.
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100.0%; Score 118; DB 7; Length 1:
Best Local Similarity 100.0%; Pred. No. 4.3e-19;
Matches 118; Conservative 0; Mismatches 0; Indels
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                                                                                                                                 Seguence 118 BP; 49 A; 14 C; 15 G; 40 T; 0 U; 0 Other;
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111. .124
*tag= d
175. .211
/rpt_type= DIRECT
175. .190
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Claim 6; Page 55; 58pp; English
                                                                                                                                                                                                                                                                                                  ABZ75335 standard; DNA; 244 BP
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111. .142
/*tag= c
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                                         A composition comprising recombinase TmpI and the recombination substrate TRT or TRT' sequences, useful for genetic engineering, TmpI-mediated genetic recombination, or for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 TAATACAACACAATATTAATTGTGTTGTATTAGGTGTTATAATAATATAAATCTAGGGG 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 TITAACGCAACACATITATCGATAAATAATACTTTTAGACGCAACACAATTTATAG 228
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Tmp1 recognised target, TRT'', ds.
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100.0%; Score 118; DB 7; Length 244;
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'bound_moiety= "TnpI"
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'note= "Tn4430 left
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                                                                                                                                                            Claim 6; Fig 1A; 58pp; English
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176. .191
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74. .193
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WPI; 2003-221599/21
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             repeat_unit
                                                                         16-JAN-2003
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                                                                                                                                                                                                               A composition comprising recombinase TnpI and the recombination substrate TRT or TRT' sequences, useful for genetic engineering, TnpI-mediated genetic recombination, or for gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B. thuringiensis TnpI recognition target TRT' functional variant #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TnpI, gene therapy; recombinase; TRT; TRT'; genetic engineering;
TnpI recognised target; TRT''; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 100.0%; Score 118; DB 7; Length 249; Local Similarity 100.0%; Pred. No. 4.4e-19; nes 118; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 249 BP; 103 A; 38 C; 36 G; 72 T; 0 U; 0 Other;
 /bound_moiety= "TnpI"
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                                                                                                                           EURO MOLECULAR BIOLOGY LUNIV CATHOLIQUE LOUVAIN.
                                                                                                                                                                                                                                                                  Claim 1; Page 55; 58pp; English.
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                                                                                                   30-JUN-2001; 2001US-00895435
                                                                           28-JUN-2002; 2002WO-EP007176
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65. .116
/*tag= c
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*tag= a
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                                                                                                                                                               Zhang Y,
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The invention relates to a novel composition comprising an isolated DNA molecule comprising TnpI recombination substrates. The composition may have a use in gene therapy, and as a vaccine. The recombinate TnpI and the recombination substrates TTP or TRT' sequences are useful for genetic engineering. The kits are useful for TnpI-mediated genetic recombination. The TnpI-mediated site-specific recombination is useful. for delating or inserting DNA sequences to medilate gene expression, integrating new nucleotide sequences into a DNA molecule, such as an episome or genomic DNA, for gene therapy, or for producing food-grade genetically modified organisms. The present sequence represents a TnpI recognised target (TRT) functional variant TRT'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A composition comprising recombinase TmpI and the recombination substrate TRT or TRT' sequences, useful for genetic engineering, TmpI-mediated genetic recombination, or for gene therapy.
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Tnp1 recognised target, TRT'', ds.
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1. 32
1. 32
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/rpt type= INVERTED
1. 14
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'rpt_type= DIRECT
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Matches 115; Conserv
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ABZ75343
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                                                                                                                                                                                                                                                                                                   A composition comprising recombinase TnpI and the recombination substrate TRT or TRT' sequences, useful for genetic engineering, TnpI-mediated genetic recombination, or for gene therapy.
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TnpI recognised target, TRI''; ds.
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65. .116
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/rpt_type= DIRECT
65. .80
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(UYLO-) UNIV CATHOLIQUE LOUVAIN.
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                                                                                                                                                                                                                                            Hallet B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.9%;
                                                                                                                                                                         30-JUN-2001; 2001US-00895435.
                                                                                                                                             28-JJN-2002; 2002WO-EP007176
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Best Local Similarity 99.1
Matches 115; Conservative
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The invention relates to a novel composition comprising an isolated DNA molecule comprising Tnpl recombination substrates. The composition may have a use in gene therapy, and as a vaccine. The recombinase Tnpl and the recombination substrates TRY or TRY sequences are useful for genetic engineering. The kits are useful for Tnpl-mediated genetic recombination. The Tnpl-mediated site-specific recombination is useful for deleting or inserting DNA sequences to modulate gene expression, integrating new nucleotide sequences into a DNA molecule, such as an episome or genomic or gene therapy, or for producing food-grade genetically modified organisms. The present sequence represents a Tnpl recognised target (TRT) functional variant TRY
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Inpl recognised target; TRT'; ds; consensus.
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Pred. No. 2.6e-06;
0; Mismatches 52; Indels

    B. thuringiensis Inpl recognition target TRT consensus.

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1. .32
/ tag= b
65. .116
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Best Local Similarity 55.2%;
Matches 64; Conservative
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Homo sapiens
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Local Similarity 65.6%; Pred. No. 0.003;
es 82; Conservative 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 124 BP; 36 A; 13 C; 7 G; 26 T; 0 U; 42 Other;
       /rpt_type= INVERTED
1. 14
4.tag= b
75. 124
/*rag= c
/*rpt_type= DIRECT
75. 89
                                                                                                                                                                 BIOLOGY LAB.
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                                                                                                                                                                MOLECULAR BIOLOGY L
CATHOLIQUE LOUVAIN.
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633 TAATACAAAACAAACATATTTATATTAAATATTAGTTTTAATAAGCTAATTTCATGTT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TAATACAACACAATATTAATTGTGTTGTATTAGGTGTTATAATAATATAAATCTAGGG 60
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                                                                                                                                                                                                                                                                                                                                                            Glazebrook J, Goff SA, Ho
Whitham S, Xie Z, Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; SEQ ID NO 6355; 899pp; English.
                                                                                                                                                                                                                                                                                                    (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                            Chang H, Chen W, Cooper B,
Katagiri F, Quan S, Tao Y,
                                                                                                                                                                              22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                            22-JUN-2001; 2001WO-IB001105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       illustrate the invention
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ses 70; Conserv
                                                       WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression
Oryza sativa.
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Danchin A;

Kunst F,

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om base 30001 (Photorhabdus luminescens nuclectic
Locus ACF65385 Accession Acf65385
                                                                                                                                                                                                                                        The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes are used for detection/identification of the genes are used for detection/identification of polypeptides encoded by the genes. Proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter cesponse or sensitivity to toxins and antibiotics produced by P. cresponse or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes proteins, vectors containing the genes and Ab are also useful are sensitive to P. luminescens and Ab are also useful as biopesticides. Other uses of the genes and the proteins are as virulence are sensitive to P. luminescens and the proteins are as virulence factors and for identifying targets of human diseases for which P. creat micropial pages and whooping cough). This sequence represents one of the isolated P. luminescens genes
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                                                                                                                    Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.2%; Score 38; DB 7; Length 750; Best Local Similarity 60.8%; Pred. No. 3.7; Matches 62; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 750 BP; 291 A; 86 C; 139 G; 234 T; 0 U; 0 Other;
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Glaser P, Frangeul L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Pred. No. 4
                                                                                                                                                                                                       Claim 2; SEQ ID NO 8699; 1205pp; French
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60.8%;
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Matches 62; Conservative
  Taourit S,
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Continuation (4 of 7) of
WP Sequence split into 7
                                                                          WPI; 2003-148459/14
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ACF65385_4
ACF65385_5
                        Buchrieser C;
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ACF65385_2
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     Duchand E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the disgnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid relukaemia, Alzhaimer's disease, Alzhailepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                           chemically modified gene, useful for associated with abnormal cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 847 TATATATTAGTTTAATATATATATAATTATAAATTTGATAATTAAGTAAGTTGT 902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 1; SEQ ID NO 1999; 32pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of diagnosis and treatment of diseases
                                                                                                                                                                                                                                                                                               Berlin K;
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(CNRS ) CNRS CENT NAT RECH SCI
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                                                                                                                                                             30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                         02-JUL-2001; 2001WO-EP007537
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ses 68; Conservative
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                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
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                                                          03-JAN-2002
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DB 7; Length 110000;

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RESULT 14

ACEG7367 33.C

CONTINUATION (34 of 57) of ACEG7367 from base 3300001 (Photophabdus luminescens nuclei wp Sequence split into 57 fragments incourse incourse incourse and the Aceg7367 
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0; Mismatches
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Best Local Similarity burgery 62; Conservative
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ACCENTATION 13

                                               ACF65385 from base 400001 (Photorhabdus luminescens nucleotide fragments LOCUS ACF65385 Accession Acf65385 Begin End
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ilarity 60.8%;
Conservative
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RESULT 12
ACF65385 4/c
Continuation (5 of 7) of AC
WP Sequence split into 7 fix
WP ACF65385 0
WP ACF65385 1
WP ACF65385 3
WP ACF65385 3
WP ACF65385 4
WP ACF65385 5
WP ACF65385 5
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Best Local Simil
Matches 62;
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Search completed: February 28, 2004, 07:22:24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                              7 AACACAAHATHAATHGHGHTGHATHAGGHGHTAHAAHAAAHAHAAAHCHAGGGGHTHAAC 66
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                                                                                                                                                                                                                                                                                                         67 GCAACACAATTTATCGATAAATAAATACTTTTAGACGCAACA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune system associated gene SEQ ID NO: 2000.
                                                                                                                                                                                                                                       0; Mismatches
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Pred. No.
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01-SEP-2000; 2000DE-01043826
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzoiemer's disease, Alzo, spilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TITAACGCAACACAATITATCGATAAATAATACTTTTAGACGCAACACAATITAT 116
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Best Local Similarity 57.8%;
Matches 67; Conservative
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Sequence 2, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 1999, Ap
Sequence 2000, Ap
Sequence 313, App
Sequence 313, App
Sequence 21, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 23, Appli
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/DEM_PUBM_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-895-435-1
US-09-895-435-4
US-09-895-435-4
US-09-895-435-8
US-09-895-435-9
US-09-895-435-9
US-10-311-455-1999
US-10-311-455-1999
US-10-311-455-333
US-10-311-455-333
US-10-311-455-333
US-10-311-455-333
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US-10-081-051-233
US-10-081-051-23
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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	APPLIC	ANT:	Stew	art	A. F.								
	APPI.TO	ANT:	Zha	b.	X								
	APPLICANT:	ANT	r. Hallet,	let.	m								
	TITLE	OF IN	VENT	NOI	A New	Tyr	ë	Recombinase	for	Genetic	Engineering	ring	
	FILE R	REFERENCE	NCE:	988	2-012-	666							
٠.	CURRENT	T APE	PLICATION	TIO	NUMBE	R: US,	,709/895,	,435					
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Sequence 1, Application US/09895435 Publication No. US20030113837A1 GENERAL INFORMATION:

RESULT 2 US-09-895-435-1 . 0

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96.9<del>%</del>;
99.1%;
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Best Local Similarity 99.1
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NUMBER OF SEQ ID NO
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APPLICANT: Stewart, Y.
APPLICANT: Zhang, Y.
APPLICANT: Hallet, B.
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
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CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT FILING DATE: 201-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 249
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                                                 APPLICANT: Zhang, Y.
APPLICANT: Hallet, B.
TITLE NOT INVENTIOR. A New Tyrosine Recombinase for Genetic Engineering
FILE REFERENCE: 9882-012-999
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Pred. No. 3.8e-18;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 118; DB 10;
; Pred. No. 3.7e-18;
0; Mismatches 0;
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Publication No. US20030113837A1
GENERAL INFORMATION:
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CRGANISM: Bacillus thuringiensis
US-09-895-435-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 118; Conservative 0;
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Best Local Similarity 100.0%;
Matches 118; Conservative 0
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APPLICANT: Stewart, A. F.
APPLICANT: Lang, Y.
APPLICANT: Lang, Y.
APPLICANT: Allet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REFERENCE: 9882-012-999
FILE REFERENCE: 9882-012-999
CURRENT APPLICATION UNMER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 116
                                                                                                                                                                                                                                                                                                             61 TITAACGCAACACAATTTATCGATAAATAATACTTTTAGACGCAACACAATTTAT 116
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Publication No. US20030113837A1
Publication No. US2003113837A1
ENERRAL INFORMATION:
APPLICANT: Shewart, A. F.
APPLICANT: APPLICANT: Alang, Y. F.
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REPERENCE: 9882-012-99
CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
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                                                                                                    Length 116;
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96.9%; Score 114.4; DB 10
Best Local Similarity 99.1%; Pred. No. 2.1e-17;
Matches 115; Conservative 0; Mismatches 1.
                                                                                                         Score 114.4; DB 1
Pred. No. 2.1e-17;
                                                                                                                                                          0; Mismatches
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; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-895-435-7
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Length 761;
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Pred. No. 1.9;
0; Mismatches 39;
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33.2%; Score 39.2; DB 14;
Best Local Similarity 58.6%; Pred. No. 15;
Matches 68; Conservative 0; Mismatches 48;
                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_95242C.1
US-10-424-599-137579
    FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 137579
LENGTH: 761
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Best Local Similarity 62.5%;
Matches 65, Conservative (
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ORGANISM: Artificial Sequence
                                                                                                                            TYPE: DNA ORGANISM: Glycine max
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US-10-311-455-2000/c
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, Y.
APPLICANT: Stewart, Y.
APPLICANT: Chang, Y.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT PILING DATE: 2011-06-30
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch
    43.2%; Score 51; DB 10; Length 124;
1 Similarity 65.6%; Pred. No. 0.0082;
82; Conservative 0; Mismatches 32; Indels
                                                                                                                                                                     Score 64; DB 10; Length 116;
Pred. No. 8.2e-06;
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Publication No. US20030113837A1
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NAME/KEY: N region
LOCATION: 33 .. 64
OTHER INFORMATION: n = a, t, g,
NAME/KEY: N region
LOCATION: 81 .. 100
OTHER INFORMATION: n = a, t, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin version 3.0 SEQ ID NO 10
                                                                                                                                                                   Query Match
Best Local Similarity 55.2%;
Matches 64; Conservative
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NAME/KEY: N region
LOCATION: 33 .. 74
OTHER INFORMATION: n = a,
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Matches 82, Conserv
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Sequence 1999, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BIEPENBROCK, Christian

APPLICANT: BIEPENBROCK, Christian

APPLICANT: BIENIN, Kurt

TITLE OF INVENTION: Cytosine methylation

FILE REPREBRUE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NOS: 2424
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                                                                                                               632 AAACCATTTTATATTTTTTTTTAGAAGGTGGAATAAACAAAGATTTACCGGTTTTCCC 691
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                                                    TITAACGCAACACAATITATCGATAAATAATACTTTTAGACGCAACACAATITAT 116
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Gaps
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; CTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1999
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Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
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Query Match
Best Local Similarity 56.5%;
Matches 65; Conservative
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Matches 61; Conservative
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APPLICANT: OLEK, Alexander
APPLICANT: DLEK, ALExander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kuxt
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: US/20/212-16
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER: OF SEQ ID NOS: 2424
APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ

TITLE OF INVENTION: Cytosine methylation

FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR PRILING DATE: 2001-07-02

PRIOR PLING DATE: 2000-06-30

PRIOR PLING DATE: 2000-06-30

PRIOR PLING DATE: 2000-06-30

PRIOR PLING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NOS: 2424
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                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 31.9%; Score 37.6; DB 14; Best Local Similarity 57.8%; Pred. No. 36; Matches 67; Conservative 0; Mismatches 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 58; Conserv
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Sequence 313,349plication US/10311455
; Sequence 313, Application Wo. US20030143666Al
GENERAL INFORMATION:
APPLICANT: OLEK, ADEXANDER:
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete
TITLE OF INVENTION: UNDER: US/10/311,455
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
SEQ ID NOS: 2424
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Sequence 110450, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 110450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 acacaanaacaacirirahaarrahaarrahirahceraaraahaarahaaaaraaaar 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 ACACAATATTAATTGTGTTGTATTAGGTGTTATAATAATATAAATCTAGGGGTTTAACG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AATACAACACAATATTAATTGTGTTTGGTGTTTATAATAATATAAATCTAGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 CAACACAATITATCGATAAATAATACTTTTAGACGCAACACAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 TACCACTATTAAATCATAAAAAAAAACTTAACAAAAAATACAA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_70748C.1 US-10-424-599-110450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.8%; Score 35.2; DB
58.7%; Pred. No. 93;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 1
Pred. No. 56;
0; Mismatches
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*BATURE:
NAME/KEY: misc_feature
LOCATION: (8233)..(8235)
OTHER INFORMATION: Inverse complement of MGC5302 translation initiation codon (AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
COCATION: (801<u>3</u>)..(8312)
OTHER INFORMATION: Genomic fragment identified as part of CpG island (Genbank 259
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (901<u>9</u>)..(9033)
OTHER INFORMATION: BIVM Exon A alternative splice donor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (16833)..(16835)
OTHER INFORMATION: BIVM translation initiation codon (ATG)
                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (3164)..(3366)
OTHER INFORMATION: Inverse complement of MGC5302 Exon
                                                                                                                                                                                 LOCATION: (2904)..(2985)
OTHER INFORMATION: Inverse complement of MGC5302 Exon
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (6395)..(6570)
OTHER INFORMATION: Inverse complement of MGC5302 Exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAME/KEY: misc_feature
LOCATION: (8059)..(8572)
DTHER INFORMATION: Inverse complement of MGC5302 Exon
                                     LOCATION: (823)..(997)
OTHER INFORMATION: Inverse complement of MGC5302 Exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AME/KEY: misc feature
LOCATION: (14862) ..(14876)
THER INFORMATION: BIVM Exon B splice acceptor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (16701)..(16715)
OTHER INFORMATION: BIVM Exon 1 splice acceptor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (14946)..(14960)
OTHER INFORMATION: BIVM Exon B splice donor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (17301)..(17315)
OTHER INFORMATION: BIVM Exon 1 splice donor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
OCATION: (9077)..(9091)
OTHER INFORMATION: BIVM Exon A splice donor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (14872)..(14955)
OTHER INFORMATION: BIVM Exon B - untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
.OCATION: (8614)..(9086)
.THER INFORMATION: BIVM Exon A - untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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NAME/KEY: misc_feature
NOCATION: (16711)..(17310)
OTHER INFORMATION: BIVM Exon 1
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OCATION: (16309)..(16309)
THER INFORMATION: n = a,
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NAME/KEY: misc_feature
                                                                                                                                                NAME/KEY: misc feature
LOCATION: (2904)..(2989
NAME/KEY: misc_feature
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US-10-417-476-3/C

Sequence 3, Application US/10417476

Sequence 3, Application US/2040002102A1

GENERAL INFORMATION:

APPLICANT: Litman, Gary W.

APPLICANT: Hawke, No. US20040002102A11 A.

APPLICANT: Beaon, Donna D.

TITLE OF INVENTION: Transcriptional Products, and Uses Thereof

TITLE OF INVENTION: Transcriptional Products, and Uses Thereof

CURRENT APPLICATION NUMBER: US/10/417,476

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LEAGTH: 96898
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barbet, Anthony F.
APPLICANT: Whitmire, William M.
APPLICANT: Whitmire, William M.
APPLICANT: Simbi, Bigboy H.
APPLICANT: Simbi, Bigboy H.
APPLICANT: Simbi, Bigboy H.
APPLICANT: Moreland, Annie L.
APPLICANT: Moreland, Annie L.
APPLICANT: Manang, Duncan M.
APPLICANT: Manang, Suman M.
APPLICANT: Manang, Suman M.
APPLICANT: Mahan, Mahan, Suman M.
APPLICANT: Mahan, Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              950 CTTAATCATTACACTTTATGTATATTACAAATTTTTGAACAATAATAAATTAAA 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AATACAACACAATATTAATTGTGTTGTATTAGGTGTTATAATAAAATATAAATCTAGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 ITAACGCAACACAATITATCGAIAAAIAAATACTITITAGACGCAACAATITATA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                         TTAACGCAACACAATTTATCGATAAATAATACTTTTAGACGCAACACAATTTAT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , TYPE: DNA
, ORGANISM: Ehrlichia ruminantium (formerly Cowdria ruminantium)
US-10-081-051-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (466)...(702)
OTHER INFORMATION: Inverse complement of MGC5302 Exon FEATURE:
                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/10081051 Publication No. US20030044422A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature LOCATION: (466)..(702)
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LENGTH: 2778
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us-09-895-435a-2.rnpb

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TAME/KEY: misc feature
OCATION: (44021)..(44035)
THER INFORMATION: BIVM Exon 7 splice acceptor site
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OCATION: (411<u>2</u>0)..(41134)
OTHER INFORMATION: BIVM Exon 6 splice acceptor site
LOCATION: (25983)..(25997)
OTHER INFORMATION: BIVM Exon 2 splice acceptor site
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
OCATION: (31620)..(31634)
OTHER INFORMATION: BIVM Exon 5 splice acceptor site
                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (30592)..(30606)
JTHER INFORMATION: BIVM Exon 3 splice acceptor site
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AME/KEY: misc_feature
LOCATION: (31290)..(31312)
OTHER INFORMATION: BIVM Exon 4 splice acceptor site
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NAME/KEY: misc_feature
JOCATION: (31715)..(31729)
OTHER_INFORMATION: BIVM Exon 5 splice donor site
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OCATION: (41253)..(41267)
THER INFORMATION: BIVM Exon 6 splice donor site
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LOCATION: (44108)..(44122)
OTHER INFORMATION: BIVM Exon 7 splice donor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAME/KEY: misc feature
OCCATION: (31403)..(31417)
OTHER INFORMATION: BIVM Exon 4 splice donor site
                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (26110)..(26124)
OTHER INFORMATION: BIVM Exon 2 splice donor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (30688)..(30702)
THER INFORMATION: BIVM Exon 3 splice donor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATURE:
|AME/KEY: misc_feature
|OCATION: (41130)..(41262)
|THER INFORMATION: BIVM Exon 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
COCATION: (44031)..(44117)
OTHER INFORMATION: BIVM EXON 7
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AME/KEY: misc feature
OCATION: (31630)..(31724)
THER INFORMATION: BIVM Exon 5
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (30602)..(30697)
OTHER INFORMATION: BIVM Exon 3
                                                                                                NAME/KEY: misc_feature
LOCATION: (25993)..(26119)
OTHER INFORMATION: BIVM Exon 2
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AME/KEY: misc feature
OCATION: (31308)..(31412)
THER INFORMATION: BIVM Exon 4
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LOCATION: (48198)..(48212)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 TIAATTGTGTTGTTTAGGTGTTATAATAATATAAATCTAGGGGTTTAACGCAACACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (49428)..(49430)
OTHER INFORMATION: BIVM translation termination codon (TGA)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.2%; Score 34.4; DB 15; Length Best Local Similarity 59.0%; Pred. No. 3e+02; Matches 59; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81198 irraharahahahahacahahgrahdrahahahah 81159
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                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (49127)..(49141)
OTHER INFORMATION: BIVM Exon 9 splice acceptor site
OTHER INFORMATION: BVIM Exon 8 splice acceptor site
                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (48255)..(48309)
OTHER INFORMATION: BIVM Exon 8 splice donor site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 28, 2004, 09:12:49
Job time : 131.718 secs
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LOCATION: (50039)..(50248)
OTHER INFORMATION: Alu sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (55216).. (55975)
OTHER INFORMATION: ERCCS Exon 1
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (49137)..(51096)
OTHER INFORMATION: BIVM Exon 9
                                                 NAME/KEY: misc feature
LOCATION: (48208)..(48304)
OTHER INFORMATION: BIVM Exon 8
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cgni2_6/ptodata/2/pina/US1011B_COMB.seq:

cgni2_6/ptodata/2/pna/US1011B_COMB.seq:

cgni2_6/ptodata/2/pna/US1013B_COMB.seq:

cgni2_6/ptodata/2/pna/US1013B_COMB.seq:

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cgni2_6/ptodata/2/pna/US1016_COMB.seq:

cgni2_6/ptodata/2/pna/US1016_COMB.seq:

cgni2_6/ptodata/2/pna/US1016_COMB.seq:

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cgni2_6/ptodata/2/pna/US5001_COMB.seq:

cgni2_6/ptodata/2/pna/US6013_COMB.seq:

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cgni2_6/ptodata/2/pna/US6023A_COMB.seq:

cgni2_6/ptodata/2/pna/US6023A_COMB.seq:

cgni2_6/ptodata/2/pna/US6023A_COMB.seq:

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3: /cgn2_6/ptodata/2/pna/USO6_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/USO8_COMB.seq:*
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Minimum Maximum

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% Query Match	00000	96	0 0 0 0 0 4 0 0 0	10 4.4 14 4.4 10 6.4	. W W W . W W R . W W R		2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	333.1 1.1.0	31.7	31.4	31.4 31.4	31.2	30.8	9.00	900	30.8	30.8	30.5	30.5		pplicat MATION: tewart, Zhang, Hallet, ENTION: CC ID NG CC ID NG CC ID NG CT ID NG TentIN
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GENERAL INFORMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, B.
TILLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REPERBERGE: 9882-012-99
CURRENT APPLICATION NUMBER: 2001-06-30
CURRENT FILING DATE: 2001-06-30
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
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APPLICANT: Stewart, A. F.
APPLICANT: Stewart, Y.
APPLICANT: Allack, Y.
APPLICANT: Hallack, Y.
APPLICANT: Hallack, Y.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REPRENEUR: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOTTWARE: Patentin version 3.0
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Query Match 100.0%; Score 118; DB 36; Best Local Similarity 100.0%; Pred. No. 2.7e-17; Matches 118; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus thuringiensis
S-09-895-435-1
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S-09-895-435A-2
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S-09-895-435-1
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Sequence 7, Application US/09895435 GENERAL INFORMATION:
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                                                                                                                                                                                                                 TYPE: DNA
CRGANISM: Bacillus thuringiensis
US-09-895-435A-4
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Best Local Similarity 99.1
Matches 115; Conservative
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Best Local Similarity
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US-09-895-435-8
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US-09-895-435-7
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171 TITAACGCAACACAATITATCGATAAATAATACTITTAGACGCAACACAATITATAG 228
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CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                               APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: Hallet, B.
APPLICANT: Hallet, B.
APPLICANT: Hallet, B. New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435A
CURRENT APPLICATION NOWBER: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
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100.0%; Score 118; DB 36;
Best Local Similarity 100.0%; Pred. No. 2:9e-17;
Matches 118; Conservative 0; Mismatches 0;
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APPLICANT: Stewart, A. F.
                                                                                                                           Sequence 1, Application US/09895435A GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Bacillus thuringiensis
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LENGTH: 244
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GENERAL INFORMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Stang, Y.
APPLICANT: Hallet, B.
APPLICANT: Ballet, B.
APPLIC
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APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435A
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 249
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illarity 100.0%; Pred. No. 2.9e-17;
Conservative 0; Mismatches 0;
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99.1%; Pred. No. 1.8e
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SEQ ID NO 9
LENGTH: 116
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TYPE: DNA
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APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: Stang, Y.
APPLICANT: Hallet, B.
TITLE OF INVENTION: Now Tyrosine Recombinase for Genetic Engineering FILE REPRENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435A
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
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APPLICANT: Stewart, A. F.
APPLICANT: Stang, Y.
APPLICANT: Hallet, Y.
APPLICANT: Hallet, Y.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REFERENCE: 988-2-012-99
CURRENT APPLICATION NUMBER: US/09/695,435A
CURRENT PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
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                                                                                                       Score 114.4; DB 36; Length
Pred. No. 1.8e-16;
0; Mismatches 1; Indels
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96.9%; Score 114.4; DB 3
Best Local Similarity 99.1%; Pred. No. 1.8e-16;
Matches 115; Conservative 0; Mismatches 1
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; ORGANISM: Bacillus thuringiensis
US-09-895-435A-8
; LENGTH: 116
; TYPE: DNA
, ORGANISM: Bacillus thuringiensis
US-09-895-435-8
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Best Local Similarity 99.1%;
Matches 115; Conservative
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APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, Y.
APPLICANT: Hallet, B.
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REFERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435A
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
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APPLICANT: Anilet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
FILE REPERENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
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Pred. No. 5.8e-05;
0; Mismatches 52
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Best Local Similarity 55.2
Matches 64; Conservative
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LOCATION: 81 . 100
OTHER INFORMATION: n
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OTHER INFORMATION:
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Pred. No. 8.9;
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PRIOR FILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-26
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PRIOR FILING DATE: 2001-01-26
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PRIOR FILING DATE: 2001-06-23
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 6813
NUMBER OF SEQ ID NOS: 6813
SECTIVARE: FASESEE FOR WINDOWS VERSION 4.0
                                                                                                                                                                       1 TAATACAACACAATATTAATTGTGTTGTATTA-
                                                                                             Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
5.09-887-272A-6355/c
; Sequence 6355, Application US/09887272A
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-06-23
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                                                                                             Query Match
Best Local Similarity 65.6%;
Matches 82; Conservative
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Zhu, Tong
Whitham, Steve
Goff, Steve
Garaebrook, Jane
Chen, Wenguing
Katagiri, Fumiaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Oryza sativa
US-09-887-272A-6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hou, Yu-Ming
APPLICANT: Quan, Sheng
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Best Local Similarity
---a 70; Conserva
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                                                                                                                                                                                                                                                                                                                        111 ATTTA 115
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; NAME/KEY: N region
; LOCATION: 33 . 74
; OTHER INFORMATION:
US-09-895-435A-10
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APPLICANT: Hallet, B.
TILLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering;
FILE REPRENCE: 9882-012-999
CURRENT APPLICATION NUMBER: US/09/895,435
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
TYPE- TYPE- TYPE- TO NOS: 10
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                                                                                                                                                   --GGTGTTATAATAATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09895435A
GENERAL INFORMATION:
APPLICANT: Stewart, A. F.
APPLICANT: Stewart, A. F.
APPLICANT: Alang, Y.
APPLICANT: Hallet, B.
TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering FILE REPERENCE: 9882-012-996
CURRENT APPLICATION NUMBER: US/09/895,435A
CURRENT FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 10
SOFTHARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 124
                                                                                                                                                                                    61 TTTAACGCAACACAATTTATCGATAAATAATTACTTTTAGACGCAACACAATTTAT 116
                                                                             Gaps
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Pred. No. 0.055,
0, Mismatches 32, Indels
                                       Length 116;
                                                                             Indels
                                       Score 64; DB 36;
Pred. No. 5.8e-05;
                                                                             0; Mismatches
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LOCATION: 33 ... 74

COTHER INFORMATION: n = a, t, g, or

US-09-895-435-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Bacillus thuringiensis
                                       54.2%;
55.2%;
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Best Local Similarity 65.6%;
Matches 82; Conservative
                                     Query Match
Best Local Similarity 55.2
Matches 64; Conservative
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 US-09-895-435A-9
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                                                                                             --GGTGTTATAATAATATA 50
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DB 36; Length 124;
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TITLE OF INVENTION: PLANT GENES INVOLVED IN DEFENSE AGAINST
FITLE OF INVENTION: PATHOGENS
FILE REFERENCE: 1360.003US2
CURRENT APPLICATION NUMBER: US/09/887,272A
CURRENT FILING DATE: 2001-06-23
                                               Indels
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Search completed: February 28, 2004, 10:49:19 Job time: 1860.17 secs

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NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ 100 10805
LENGTH: 1790242
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                                                                                                                                                                                                     February 28, 2004, 07:22:37; Search time 20.2561 Seconds (without alignments) 981.354 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                       118
1 taatacaacacaatattaat.....agacgcaacacaatttatag 118
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1: /cgn2 6/ptodata/1/pna/USO6 NEW COMB.seq:*

2: /cgn2 6/ptodata/1/pna/USO7 NEW COMB.seq:*

4: /cgn2 6/ptodata/1/pna/USO7 NEW COMB.seq:*

4: /cgn2 6/ptodata/1/pna/USO8 NEW COMB.seq:*

5: /cgn2 6/ptodata/1/pna/USO8 NEW COMB.seq:*

6: /cgn2 6/ptodata/1/pna/USO8 NEW COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USO8 NEW COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USO8 NEW COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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6 US-10-767-471-10805
6 US-10-767-471-10805
6 US-10-767-471-10805
6 US-10-767-471-10805
6 US-10-767-471-10713
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6 US-10-767-471-10715
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6 US-10-767-471-10714
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Maximum Match 100%
Listing first 45 summaries
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26.6 1790242 6
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51995 6
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Match Length DB
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Perfect score:
Sequence:
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C 27 27.8 23.6 201 6 US-10-767-471-23856 Sequence 23856, A 29.2 27.8 23.6 18856 6 US-10-767-471-10647 Sequence 10647, A 29.2 27.8 23.6 188053 6 US-10-755-790-5 Sequence 5, Appli Sequence 27.8 23.6 546055 6 US-10-755-790-5 Sequence 10717, A 20.2 23.6 546055 6 US-10-757-71-10717 Sequence 10717, A 20.2 23.4 201 6 US-10-767-471-40250 Sequence 10777, A 20.2 23.4 1899 6 US-10-767-70-17975 Sequence 2007, Appli 27.6 23.4 1899 6 US-10-767-70-17975 Sequence 2007, Appli 27.6 23.4 1899 6 US-10-767-70-17975 Sequence 27.7 Appli 27.6 23.4 16329 6 US-10-765-790-27 Sequence 107130, A 27.6 23.4 16329 6 US-10-767-471-10616 Sequence 10016, A 27.4 23.2 1157 6 US-10-767-471-444 Sequence 10016, A 27.4 23.2 1157 6 US-10-767-471-444 Sequence 10016, A 27.4 23.2 1157 6 US-10-767-471-10616 Sequence 10016, A 27.4 23.2 165020 6 US-10-767-471-10805 Sequence 10806, A 27.4 23.2 166020 6 US-10-767-471-10806 Sequence 10808, A 27.4 23.2 265113 6 US-10-767-471-10808	RESULT 1 US-10-76-471-10717/c   Sequence 10717, Application US/10767471   GENERAL INFORMATION: Application US/10767471   GENERAL INFORMATION: GENERAL OF CAGAILL, Michele et al.   TITLE OF INVENTION: GENERAL CROUSES   TITLE OF INVENTION: GENERAL CROUSES   TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF   TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF   CURRENT PELICATION NUMBER: US/10/767,471   CURRENT PELICATION NUMBER: US/10/767,471   SEQ ID NO 10717   SEQ ID NO 10717   LENGTH: S46025   TYPE: DAA	Duery Match  26.6%; Score 31.4; DB 6; Best Local Similarity 57.7%; Pred. No. 12; Matches 56; Conservative 0; Mismatches 41;  2 AATACAACAATATTAATTGTGTGTATTAGGTGTTATA  545424 AATACAACATTAGTTTGTTTATTTACTGTTATT  62 TTAACGCAACAATTATTGTTTGTTTATTTACTGTTATT  62 TTAACGCAACAATTATTGTTTGTTTATTTTTTTTTTTTT	. i
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NAME/KEY: misc_feature; LOCATION: (1)...(36106)
COCATION: (1)...(36106)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables US-10-767-471-10713
                                                                                                                                                                                                                                                                                                                                                 RESULT 5

US-10-767-471-10713/C

US-10-767-471-10713/Application US/10767471

SEQUENCE 10713, Application US/10767471

SEQUENCE 10713, APPLICANTION:
APPLICANTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TILLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

FILE REPRESURE: C1001505

CURRENT APPLICATION NUMBER: US/10/767,471

CURRENT FILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 50231

SOFTWARE: FASESEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01505
CURRENT EPLING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FagtSEQ for Windows Version 4.0
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                                                                                                               17 TAATTGTGTTGTATTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGCAACACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 TAATTGTGTTGTATTAGGTGTTATAATAATATAAATCTAGGGGTTTAACGCAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.9%; Score 30.6; DB 6; Length 36106; Best Local Similarity 56.4%; Pred. No. 17; Matches 57; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 51995;
        Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 TTATCGATAAATAAATACTTTTAGACGCAACAAATTTATA 117
Score 30.6; DB 6;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
25.9%; Score 30.6; Di
Best Local Similarity 62.3%; Pred. No. 18;
Matches 48; Conservative 0; Mismatches
                                                            0; Mismatches
                                                                                                                                                                                                                                                                          176 rraraaircagicarra 192
        25.9%;
                                                                                                                                                                                                                      77 TTATCGATAAATAAATA
        Query Match
Best Local Similarity 62.33
Matches 48; Conservative
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LENGTH: 36106
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                                                                                                               ; LOCATION: (1).T. (1790242)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-767-471-10805
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILLING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38439
LENGH': 201
                                                                                                                                                                                                                                                                                                                                                                                    1587671 ATTTAATGAAATATGATTCAGTAATAAAAAGGAATAAATTTGATTAAAGGAACAATATT 1587612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
SEQ ID NO 20322
LENGTH: 641
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                                                                                                                                                                                                                                                                                                                                   19 ATTGTGTTGTATTAGGTGTTATAATATATAAATCTAGGGGTTTAACGCAACAATTT
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US-10-767-701-20322
                                                                                                                                                                                                                         Score 31.4; DB 6; 3
Pred. No. 12;
0; Mismatches 31;
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26.1%; Score 30.8; DB
Best Local Similarity 55.7%; Pred. No. 14;
Matches 59; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          79 ATCGATAAATAAATACTTTTA 99
                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.7%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Sorghum bicolor
                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                        NAME/KEY: misc_feature
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GENERAL INFORMATION:
Sequence 10714, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENERIC POLYMORPHISMS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001505
CURRENT PELLING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 10714
LENGTH: 99445
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                                                                                                                                                                                                                            287 TTTTTAAGCTGATATGAGCTATAAAACGCTAAAAGGAATAAGGCAGTGGATTATATATGAAG
                                                                                                                                                        26 TGTATTAGGTGTTATAATATAAATCTAGGGGTTTAACGCAACACAATTTATCGATA 85
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                                                                                0; Gaps
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    DB 5; Length, 1047;
                                                                                Indels
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                                                                            31;
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Pred. No. 30;
0; Mismatches 39;
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    Score 30.4; DB Pred. No. 18; 0; Mismatches
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                                                                                                                                                                                                                                                                                                        86 AATAAATACTTTTAGACGCA 105
                                                                                                                                                                                                                                                                                                                                                                                227 AATAGATIGITITCIGACGIA 208
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Best Local Similarity 57.6%;
Matches 53; Conservative
Query Match
Best Local Similarity 61.2%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-767-471-10714
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FILE REPERENCE: PA481US
FILE REPERENCE: PA481US
CURRENT PEPLICATION NUMBER: US/09/830,230A
CURRENT FILING DATE: 2001-09-27
PRIOR PEPLICATION NUMBER: US/09/830,230A
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1997-09-03
PRIOR FILING DATE: 1997-09-03
PRIOR FILING DATE: 1997-07-22
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TILE OF INVENTION: Lyme Disease Vaccines
TILE REPERINCE: P8481US
CURRENT APPLICATION NUMBER: US/09/830,230A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: PCT/US98/12718
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1997-00-3
PRIOR PLING DATE: 1997-07-22
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Pred. No. 17
                                                                                                                                                                                                                                                                                                Sequence 256, Application US/09830230A GENERAL INFORMATION:
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                                        77 TTATCGATAAATAATA 93
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Best Local Similarity 61.2%;
Matches 49; Conservative
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, ORGANISM: Homo sapiens
US-09-830-230A-255
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US-09-830-230A-256
                                                                                                                                                                                                                                                            US-09-830-230A-256/c
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Sequence 695, Application US/10451467A

GENERAL INFORMATION:
APPLICANT: EBERHARDT, INES
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APPLICANT: EBERHARDT, INES
APPLICANT: BERKHARDS, EBERNARS, EBERNARS, EBERNARS, EBERNARS, EBERNARS, TITLE OF INVENTION: ASAT AND FUNCI
TITLE OF INVENTION: YBAST AND FUNCI
FILE REPREBENCE: JAB-1667
CURRENT APPLICATION NUMBER: EP 00870318.3
FRIOR APPLICATION NUMBER: EP 01870002.1
FRIOR APPLICATION NUMBER: EP 01870002.1
FRIOR APPLICATION NUMBER: EP 01870003.9
FRIOR APPLICATION NUMBER: EP 01870003.9
FRIOR APPLICATION NUMBER: EP 01870003.9
FRIOR ETLING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: PALENTING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SEQ ID NO 695
LENGTH: 884
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54.1%;
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Best Local Similarity
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SEQUENCE 10658, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, MICHEL et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILLE OF INVENTION: REPENDATION SET THEREOF
FILE REFERENCE: CLO01505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT APPLICATION NUMBER: US/04-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: PASKES FO FO WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                             ## TITLE OF INVENTION: Process for identifying chemical active ingredients and TITLE OF INVENTION: active ingredients for inhibiting the TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate blosynthesis pathway FILE REPERBNCE: 15514

TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate blosynthesis pathway CURRENT FILING DATE: 2002-06-07

CURRENT APPLICATION NUMBER: US/09/673,389A

CURRENT APPLICATION NUMBER: DE19843279.8

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1998-09-22

PRIOR FILING DATE: 1998-09-22

PRIOR FILING DATE: 1998-06-09

PRIOR FILING DATE: 1998-06-09

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PRIOR FILING DATE: 1998-07-15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 AIATTAATTGTGTTTAGGTGTTATAATAAATATAAATCTAGGGGTTTAACGCAACA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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12090 GCTGCACATAATTGTGCAATTCATATTTAC 12061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3449 CATATCAACAATTGAAAAAGAAT 3427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 CAATITATCGATAAATAATACT 95
                                                                                                                                                                                           Sequence 3, Application US/09673389A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 59.0%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (126)..(3740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: gene
LOCATION: (1)..(3872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , LOCATION: (1)..(3872)
US-09-673-389A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-767-471-10658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3872
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// LOCATION: (1)...(25346)

// COTER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-767-471-10575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10575, Application US/10767471
GENERAL INFORMATION:
APPLICANT CARGILL, Michel et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEDWATOLD ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25346
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13412, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al TILE OF INVENTION: GENERAL TITLE OF INVENTION: GENERAL POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEDMATOLD ARTHRITIS, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13412
LENGTH: 201
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                                                                                                                                   368 TAAAICTICAGCATIGIAAITITITITACTAIGITITIGATATAAAITICAGCICITITITGIIG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
       0; Gaps
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                                                                                                                                                                                                      61 TITAACGCAACACATITATCGATAAATAAATACTITTAGACGCAACACAA 111
                                                                                                                                                                                                                                                                  308 ritharcaraaracraaarcaaragacagaracagaragaaaga
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24.7%; Score 29.2; DB 6; Length 25346;
Best Local Similarity 57.8%; Pred. No. 36;
Matches 52; Conservative 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 201;
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   51; Indels
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Pred. No. 32;
0; Mismatches 38;
       0; Mismatches
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57.8%;
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Best Local Similarity 57.8<sup>3</sup>
Matches 52, Conservative
       60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-767-471-13412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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US-10-767-471-10575/c
                                                                                                                                                                                                                                                                                                                                                                                                  US-10-767-471-13412/c
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       Matches
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(265113)
JERRINORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-767-471-10658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature

| LOCATION: (1)...(1126118)

| OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-767-471-10615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10615, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEDMATOD ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT APPLICATION NUMBER: US/10/767,471
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10615.
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                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                  Query Match

24.2%; Score 28.6; DB 6; Length 265113;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 55; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230163 AGCACTTCATATTCATTTACTAAATTATTTTATAC 230201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 AACGCAACACAATTTATCGATAAATAAATACTTTTAGAC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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US-10-767-471-10615/c
SEQ ID NO 10658
LENGTH: 265113
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Db 710818 ATAAACAGAATTCTGCATGAGCTGGAAATAATACTACACTTGAGAATGAAGGAA 710759

QY 63 TAACGCAACACAATTTATCGATAAATAAATAAATTTTAGACGCAACACAATTTATA 117

Db 710758 TTTGACTATAGACTTTCTGGCCAAATAAATACTCTGCGAAGCCACTACAATAACA 710704

Search completed: February 28, 2004, 10:50:41 Job time: 29.2561 secs

us-09-895-435a-2.rst

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BM891761 sam43fll.
AV882598 AV882598
BX377054 BX377054
BH986499 ocilOh12.
                                                                                 February 28, 2004, 07:05:57; Search time 1392.53 Seconds (without alignments) 2530.460 Million cell updates/sec
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                                                                                                                                                                118
1 taatacaacacaatattaat.....agacgcaacacaatttatag 118
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                                                                                                                                                                                                                                                                                           55026578
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                          27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 BM891761
9 AV882598
13 BX377054
28 BH986499
                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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gb_htc:*
gb_htc:*
gb_est4:.*
gb_est5:.*
em_est6in:*
em_gss_hum:*
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em gss phg: *
em gss vrl: *
gb gss1: *
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Maximum DB seq length: 200000000
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2: em_esthum..*
3: em_estin...
4: em_estin...
5: em_estov.:.
6: em_estov.:.
7: em_estor...
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Match Length DB
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565
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33.2
33.2
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39.2
39.3
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Perfect score:
                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                          Searched:
                                                                                      Run on:
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040000000000000000000000000000000000000	CF606387 FOGLI02 CD74159 WY8197H06 BF043295 BP250016B CD007321 WY8076A09 CD004834 WY8042F08 CD004834 WY8042F08 CD005930 WY8060H08 CD0065930 WY8060H08 CF762291 CES000543 CF762291 CES000543 CD009553 WY8090D04 CD009553 WY8094D06 CD713887 WY8094D06 CD713887 WY8194H09 CD009615 WY8094D06 CD71387 WY8194H09 CD009615 WY8094D06 CD71387 WY8194H09 CD009615 WY8094D06 CD71387 WY8194H09 CD009615 WY8194H09 CD006026 WY8062H12 BH133166 BWTW92TR CG204053 PUISFSQTB CG172162 PUJETS4TB CG762030 PUJWBTF4TB CG762030 PUJWBTT8	TS  MRNA linear EST 11-MAR: cDNA clone SOYBEAN CLONE ID: ophyta; Embryophyta; Tracheoph	apilionoideae; ling,J., Coryell i., Kucaba,T., N., Theising, E.M., Page,D., Jackson,Y., Can Project Louis, MO 63108
BX361166 AQ258984 CG2559325 CG456613 CG456613 CG367547 CG16679 BJ36804 BJ36804 BJ36803 AZ144898 CD718817 CD006182 AQ450336 CG3256812 CG3256812 CG327867	CF606387 CF606387 CD0714159 BF042159 CD007820 CD0078301 CD008834 CD008855 CD008555 CD008555 CD008555 CD0085563 CD0085563 CD008563 CD008563 CD008563 CD008563 CD008563 CD008563 CD008563 CD008563 CD008563 CD008563 CD008563 CD008563 CD008563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563 CD0086563	ALIGNMENTS 420 bp Glycine max c NA sequence. 873 0 1120pyta; eudi	Fabales; Fab Marra,M., H Marra,M., H Marra,M., H Swallock, K., Swallock, T., Kohn, S., S Yeject Yeject Yeject Yeject Yeject Yeject Yeject
10010011848888748666	7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	m-c1068 5', mRJ I:19346' soybean,	cosids I; Fabale to 420) t, Keim,P., Vod Bolla,B., Marra lie,T., Underworserson,B., Kohr Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Waterston,R. ar Peroject Park Parkway,
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10098749999999999999999999999999999999999	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 BM891761 LOCUS DEFINITION 8 ACCESSION B VERSION B KEYWORDS SOURCE ORGANISM S	REFERENCE 1 AUTHORS SI AUTHORS K K K K K TITLE P JOURNAL U COMMENT C W W W
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Gaps

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EST 08-MAY-2003

FEATURES

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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequeré@enoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4608.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSOD1001DA06QPl&cluster=4608.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1001DA06QPl.
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BX377054 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODIO01YB12 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoffa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

1 'M.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ITAACGCAACACAATITATCGATAAATAAATACTITITAGACGCAACACAATT 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 TAACGCAACACTTTATCGATAAATAAATACTTTTAGACGCAACACA 110
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                                                                                                                                                                                                                                                                                                          Length 565;
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                                                                                                                                                                                                                                                                                                          DB 9;
'organism="Ciona intestinalis"
                                                                                                                                                                                                                                                                                                      Score 39.2; DB
Pred. No. 30;
0; Mismatches
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46.4%; Pred. No. 23;
tive 20; Mismatches
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                                                                                                                                                                                                                                                                                                          33.2%;
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Best Local Similarity
Matches 65; Conserv
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Best Local S
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BX377054
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                                                                                                                                                                                                                                                                                                                                                                    /organism="Glycine max"
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/dione="govern:3847"
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greenhouse grown"
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/note="vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The CDNA library was constructed from mRNA isolated
from drought stressed leaf tissue of the cultivar Williams
82. The month old greenhouse grown plants were deprived of
water for 3 days prior to harvesting the stressed leaf
tissue. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
                                                                     Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECORI-XhoI restriction site of the pBluescript vector. The Jaqued cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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AV882598
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1 (Dases 1 to 565)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
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Location/Qualifiers
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.3%; Score 41.6; D 62.5%; Pred. No. 10; tive 0; Mismatches
                                                                                                                                                                                                                                         Seq primer: -40RP from Gibco
High quality sequence stop: 4
Location/Qualifiers
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Department of Zoology
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Ciona intestinalis
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                                                                                                                                                                                                                                                                                                                                                  .420
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Fax:
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ORIGIN

8 엄 ò 셤 RESULT 2 AV882598 LOCUS DEFINITION

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

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FEATURES

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ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

ORIGIN

LOCUS

RESULT 4 BH986499

ACCESSION VERSION KEYWORDS SOURCE

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Buthartoideae; Oryzaee; Oryza.
1 (bases 1 to 866)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="PIACENTA COT 25-NORMALIZED"
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digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1135 AGKGGGGGTTWRAATGTTATATAAAAAAWGGTGWGAAARKAAATATGTTWWAAAR 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TTAACGCAACACATTTATCGATAAATAAATACTTTTAGACGCAACACAATTTATAG 118
                                                      Contact: Genoscope Gentre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 BVRY cedex - France Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6196.r, Contact: Feng Liang Bmail: fliang@lifetech.com URL: http://fullnagth.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CS0DI081AG03QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
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/strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ258984 linear GSS 23 nbxb0021P09r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0021P09r, genomic survey
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43.6%; Pred. No. 38;
ative 23; Mismatches 43; Indels
  Full-length cDNA libraries and normalization Unpublished (2001)
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Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI081YM05"
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Location/Qualifiers
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Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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Best Local Similarity 43.6%
Matches 51; Conservative
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                                                                                                                                                                 BH986499 713 bp DNA linear GSS 07-OCT-2002 oeilOhl2.bl B.oleracea002 Brassica oleracea genomic, genomic survey
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Anote="Vector: poTwa13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Obborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                                                                                                                                                                                                                                                                                                                                                  Brassica distracta
Brassica distracta
Brassica distracta
Braryophyta; Wilplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosida II; Brassicales, Brassicaceae, Brassica.
1 (bases I to 713)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Umpublished (2002)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Sequencing Center
Washington University School of Medicine
Brail: submissions@watson.wustl.edu
Plate: oeil0 row: h column: 12
Seq primer: -21UFpOr forward
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
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                                                                                                                                                                                                                                                                                                                                 Brassica oleracea
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SOURCE ORGANISM

REFERENCE AUTHORS

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901 bp DNA linear GSS 17-SEP-2003
Zea mays genomic clone ZMMBTa0675E14,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Papermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 901)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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/db xref="taxno:4577"
/clone="ZMMBTa0675E14"
/clone="zMMBTa0675E14"
/clone="tb="zM_0-1.0 KB"
/note="Vector: pCR4-TOFO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
                                                                                                                                                                                                                                             /clone lib="ZM_0.7_1.5 KB"
/note="Vector: pBCSK-; Site_1: HinclI; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                        Length 682;
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                                                                                                                                                                                                                                                                                                                                                        62 TTAACGCAACAATTTATCGATAAATAATACTTTTA 99
                                                                                                                                     Score 37.2; DB 29;
Pred. No. 77;
0; Mismatches 38;
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61.2%; Pred. No. 70;
tive 0; Mismatches 38;
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                                        CG259325 682 bp DNA linear GSS 25-AUG-2003 CGWKS85TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0610P01,
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
Clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Muberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
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Fax: 301-838-0208
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     clone="nbxb0021P09r"
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Class: sheared ends.
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CG259325.1 GI:34167746
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971 bp DNA linear GSS 20-AUG-2003 PUFLD31TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0675E14,
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1 (bases 1 to 971)
1 (bases 1 to 971)
Reshick, A., Quackenbush, J., Van Aken, S., Utterback, T., Reshick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
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/clone="Inb="ZM_0.6_1.0 KB"
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COT selected genomic DNA library"
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                                                                                                                                                                                                                              /db_xref="taxon:4577"
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/clone="taxmx 0.7.1.5 KB"
/clone="vector: pBcSK-; Site 1: HinclI; 0.7-1.5
methylation filtered genomic DNA library"
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Property Market Drive, Rockville, MD 20850, USA 7912 M01-838-5843
Pax: 301-838-0208
Email: whitelaw@tigr.org
                          9712 Medical Center Drive, Rockville, MD 20850, USA
1911: 301-838-5643
Fax: 301-838-0208
Email: whitelaw@tigr.org
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61.2%; Pred. No. 69;
tive 0; Mismatches
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                                                                                                                                                                        /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/mol_type="genomic DNA"
/strain="B73"
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Location/Qualifiers
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Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
Other GSSs: PUFLD31TD
Contact: Cathy Whitelaw
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CG116679.1 GI:34000116
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Best Local Similarity 61.2%
Matches 60, Conservative
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902 bp DNA linear GSS 17-SEP-2003
PUFLD31TBB ZM 0.6_1.0 KB Zea mays genomic clone ZMMBTa0675E14,
CG456613
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Spermatophyta; Mgnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
I (bases 1 to 902)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
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/strain="B73"
/db xref="taxon:4577"
/clone="ZMMBTa0675E14"
/clone="Lb="ZM 0.6-1.0 KB"
/note="Vector: pCR4-TOP60, Site_1: EcoRI; 0.6-1.0 kb high.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C.A., Chackenbush, J., Van Aken, S., Utterback, T.,
Esenick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                      Center Drive, Rockville, MD 20850, USA
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Othpublished (2003)
Other GSSs: PUFLD31TB PUFLD31TD PUFLD31TDB
Contact: Cathy Whitelaw
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Seg primer: TR
Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: whitelaw@tigr.org
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Contact: Cathy Whitelaw
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Tel: 301-838-5843
Fax: 301-838-0208
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les 60; Conserv
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CG367547
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By 191 91006 EVRY cedex - FRANCE [E-mail : segref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gosegawa and Maron Mammoser in Pietre de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-38 and was constructed by partial Ecor digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: or bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hypridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.4%; Score 37; DB 29; Length 928; 32.5%; Pred. No. 77; ive 37; Mismatches 42; Indels
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Department of Eukaryctic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 938 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
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/clone lib="RRCI-98"
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Rattus norvegicus
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BH358603.1 GI:17289337
   1 (bases 1 to 928)
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les 38; Conservative
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BH358603/c
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ALO71865.1 GI:4948170
                                                                                                                                                                                                                                                                                                                                                                                                                    BJ369046
BJ369046 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc49h06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 531)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="mat A"
/dev_stage="Culmination stage"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
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Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 93;
0; Mismatches 35; Indels
   0; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Par: 81-559-81-6856
                                                                                                                                                                                                                                324 TTAACTTAAAATTTTAAATTTTTAAATAAATAATTTTGA 361
                                                                                                                                                                                          62 TTAACGCAACACTTTATCGATAAATAAATACTTTTA 99
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Location/Qualifiers
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EST.
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ilarity 62.4%;
Conservative (
   60; Conservative
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AZ144898 140 T7 Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic cione Plate=43 Col=1 Row=0, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   availability, please contact Pieter de Jong (pdejong@mail.cho.org) Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_endg/rat/bac_end_intro.html Plate: 163 row: N column: 14 Class: BAC end; Seg primer: T7 Class: BAC end;
                                                                                                                                                                                                                                                                                                                                         /cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/note="Vector: prARBAC2.1; Site 1: BcoRI; Site_2: BcoRI;
CHORI-230 Rat (BN/SBNH8d/MCW) BAC library produced by
Pieter de Jong"
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Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, B.H. and Hood, L.
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Eucechinoidea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
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Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
20402565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36.4; DB 28; Length 394;
Pred. No. 1.4e+02;
0; Mismatches 36; Indels 0

    483
/organism="Strongylocentrotus purpuratus"

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                                                                                                                                                                                    1. .394
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cameron, RA, Davidson, EH, Division of Biology 156-29
California Institute of Technology Pasadena California 91125, USA
Far: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: T7
Class: BAC ends
High quality sequence stop: 483.
Location/Qualifiers
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Plate: 43 row: O column:
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AZ144898.1 GI:8296801
                                                                                                                                                                                                                                                                                                                             sex="Female"
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Matches 58; Conservative
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Search completed: February 28, 2004, 09:05:52 Job time : 1396.53 secs